

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2005, 12:03:35 ; Search time 158 Seconds
(without alignments)
447.276 Million cell updates/sec

Title: US-10-030-605A-21

Perfect score: 1108
Sequence: 1 MGRIRKEDRGFGHYSCN.....PNSSVDKLAALHHHHH 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1108	100.0	197	4	AB46850
2	1066	96.2	197	4	AB46851
3	986	89.0	198	4	AB46848
4	944	85.2	198	4	AB46849
5	769.5	69.4	173	7	AD47108
6	769.5	69.4	173	7	AD47108
7	769.5	69.4	173	7	AD47114
8	769.5	69.4	173	7	AD47112
9	769.5	69.4	173	7	AD47118
10	769.5	69.4	173	7	AD47118
11	769.5	69.4	173	7	AD47118
12	769.5	69.4	173	7	AD47118
13	769.5	69.4	173	7	AD47118
14	769.5	69.4	173	7	AD47118
15	769.5	69.4	173	7	AD47118
16	769.5	69.4	173	7	AD47118
17	769.5	69.4	173	7	AD47118
18	769.5	69.4	173	7	AD47118
19	769.5	69.4	173	7	AD47118
20	769.5	69.4	173	7	AD47118
21	769.5	69.4	173	7	AD47118
22	769.5	69.4	173	7	AD47118
23	769.5	69.4	173	7	AD47118
24	769.5	69.4	173	7	AD47118
25	769.5	69.4	173	7	AD47118

ALIGNMENTS

26	320	28.9	888	8	AD44168	Ad44168
27	318.5	28.7	420	5	ABP69298	ABP69298
28	300	27.1	205	2	AAW17523	AAW17523
29	297	26.8	204	7	AD63507	AD63507
30	297	26.8	205	8	ADP22671	ADP22671
31	297	26.8	211	8	ADP22673	ADP22673
32	288	26.0	252	5	AAU11447	AAU11447
33	281.5	25.4	215	2	AAW17522	AAW17522
34	278.5	25.1	542	6	ABR41645	ABR41645
35	278.5	25.1	962	7	AD629065	AD629065
36	278.5	25.1	1723	6	ABG74680	ABG74680
37	277	25.0	250	8	ADP22669	ADP22669
38	276.5	25.0	1080	4	AAW09016	AAW09016
39	276.5	25.0	1637	4	AAW79000	AAW79000
40	276.5	25.0	2263	4	AAW79000	AAW79000
41	257	23.2	197	4	AB47135	AB47135
42	257	23.2	197	4	ABG08246	ABG08246
43	257	23.2	197	8	ADQ19127	ADQ19127
44	253	22.8	97	3	AB58947	AB58947
45	210.5	19.0	511	7	AD64185	AD64185

RESULT 1
AAB46850 standard; protein; 197 AA.
XX
XX AAB46850:
XX
XX 26-APR-2001 (first entry)
XX
XX

DE Bovine gamma-crystalline mutant protein Mu12a-His fragment.

XX Gamma-crystalline; mutant; beta-leaflet; cosmetic; bioseparation;
XX biosensor; pollution detection; pollution control; gene therapy;
XX intracellular immunization.
XX
XX

OS Bos taurus.

XX DE19932688-A1.

XX 18-JAN-2001.

XX PF 13-JUL-1999; 99DE-01032688.

XX PF 13-JUL-1999; 99DE-01032688.

XX (FIED/) FIEDLER U.

XX (RUDO/) RUDOLPH R.

XX Rudolph R, Fiedler U, Boehm G, Reimann C;

XX WPI, 2001-148304/16.

XX Mutated proteins having beta-leaflet structure and related nucleic acid,
XX PT have new or improved properties, e.g. antibody-like specific binding or
XX catalytic activity.
XX
XX

PS Claim 11; Page 18-19; 28pp; German.

XX This invention describes a novel protein (I) with beta-'leaflet'
XX structure having surface-exposed amino acids, present in at least two
XX surface-exposed beta-strands of a surface-exposed beta-leaflet. The
XX protein is altered by targeted mutagenesis so that it has new, or
XX improved, specific binding, catalytic or fluorescent properties. The
XX invention also describes (1) DNA (II) that encodes (I); (2) RNA (III)
XX derived from (II); (3) prokaryotic and eukaryotic vectors and cells that
XX contain (II) or (III), or their fragments that encode a functional region
XX of (I); and (4) method for producing (I). (I) are useful for diagnosis
XX and therapy, in cosmetics, bioseparation and biosensors, and for
XX pollution detection and control, e.g. for specific targeting of gene

CC therapy vectors and for intracellular immunization. (1) can be provided
 CC with new or improved specific antibody-like binding, catalytic or
 CC fluorescent properties, without the cost and difficulties associated with
 CC producing complete or recombinant antibodies. (1) are relatively small
 CC (20 kDa) and can be expressed with other components as multifunctional
 CC fusions. They have good stability against low pH, denaturing agents and
 CC high temperatures, conditions under which antibodies are unstable
 CC
 SQ Sequence 197 AA;
 Query Match 100.0%; Score 1108; DB 4; Length 197;
 Best Local Similarity 100.0%; Pred. No. 5.7e-110;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGRIKFKEDRGFGQHYGNSDCPNLQPYFSCRNSIRVLGCMWLYERPNOGHQYFLRR 60
 DB 1 MGRIKFKEDRGFGQHYGNSDCPNLQPYFSCRNSIRVLGCMWLYERPNOGHQYFLRR 60
 QY 61 GDYPDYQOMWGFNDISIRSCRLIPQHTGTFRRRIYERDDFRGQMSITDDCPSLQDRFHLT 120
 DB 61 GDYPDYQOMWGFNDISIRSCRLIPQHTGTFRRRIYERDDFRGQMSITDDCPSLQDRFHLT 120
 QY 121 EVHSLNVLGSGWVLYEMPSSYRGROYLLRPGEYRRYLDWGAMNAKVGSLRRVMDPFSDPNS 180
 DB 121 EVHSLNVLGSGWVLYEMPSSYRGROYLLRPGEYRRYLDWGAMNAKVGSLRRVMDPFSDPNS 180
 QY 181 SSVDKLAALAEHHHHH 197
 DB 181 SSVDKLAALAEHHHHH 197
 RESULT 2
 AAB46851
 ID AAB46851 standard; protein, 197 AA.
 AC AAB46851;
 DT 26-APR-2001 (first entry)
 XX Bovine gamma-crystalline protein WT-HIS fragment.
 DE Gamma-crystalline; mutant; beta-leaflet; cosmetic; bioseparation;
 KM biosensor; pollution detection; pollution control; gene therapy;
 XX intracellular immunization.
 OS Bos taurus.
 XX
 PN DE19932688-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 13-JUL-1999; 99DE-01032688.
 XX
 PR 13-JUL-1999; 99DE-01032688.
 XX
 PA (FIEDL) FIEDLER U.
 PA (RUDOL) RUDOLPH R.
 XX
 PI Rudolph R, Fiedler U, Boehm G, Reimann C;
 XX
 DR WPI; 2001-148304/16.
 XX
 PT Mutated proteins having beta-leaflet structure and related nucleic acid,
 PT have new or improved properties, e.g. antibody-like specific binding or
 PT catalytic activity.
 XX
 PS Claim 11; Page 19-20; 28pp; German.
 CC This invention describes a novel protein (I) with beta-'leaflet'
 CC structure having surface-exposed amino acids, present in at least two
 CC surface-exposed beta-strands of a surface-exposed beta-leaflet. The
 CC protein is altered by targeted mutagenesis so that it has new, or
 CC improved, specific binding, catalytic or fluorescent properties. The

CC invention also describes (1) DNA (II) that encodes (1); (2) RNA (III)
 CC derived from (II); (3) prokaryotic and eukaryotic vectors and cells that
 CC contain (II) or (III), or their fragments that encode a functional region
 CC of (II); and (4) method for producing (1). (I) are useful for diagnosis
 CC and therapy, in cosmetics, bioseparation and biosensors, and for
 CC pollution detection and control, e.g. for specific targeting of gene
 CC therapy vectors and for intracellular immunization. (I) can be provided
 CC with new or improved specific antibody-like binding, catalytic or
 CC fluorescent properties, without the cost and difficulties associated with
 CC producing complete or recombinant antibodies. (I) are relatively small
 CC (20 kDa) and can be expressed with other components as multifunctional
 CC fusions. They have good stability against low pH, denaturing agents and
 CC high temperatures, conditions under which antibodies are unstable
 CC
 SQ Sequence 197 AA;
 Query Match 96.2%; Score 1066; DB 4; Length 197;
 Best Local Similarity 96.4%; Pred. No. 1.8e-105;
 Matches 190; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MGRIKFKEDRGFGQHYGNSDCPNLQPYFSCRNSIRVLGCMWLYERPNOGHQYFLRR 60
 DB 1 MGRIKFKEDRGFGQHYGNSDCPNLQPYFSCRNSIRVLGCMWLYERPNOGHQYFLRR 60
 QY 61 GDYPDYQOMWGFNDISIRSCRLIPQHTGTFRRRIYERDDFRGQMSITDDCPSLQDRFHLT 120
 DB 61 GDYPDYQOMWGFNDISIRSCRLIPQHTGTFRRRIYERDDFRGQMSITDDCPSLQDRFHLT 120
 QY 121 EVHSLNVLGSGWVLYEMPSSYRGROYLLRPGEYRRYLDWGAMNAKVGSLRRVMDPFSDPNS 180
 DB 121 EVHSLNVLGSGWVLYEMPSSYRGROYLLRPGEYRRYLDWGAMNAKVGSLRRVMDPFSDPNS 180
 QY 181 SSVDKLAALAEHHHHH 197
 DB 181 SSVDKLAALAEHHHHH 197
 RESULT 3
 AAB46848
 ID AAB46848 standard; protein, 198 AA.
 AC AAB46848;
 DT 26-APR-2001 (first entry)
 XX Bovine gamma-crystalline mutant Mu12A protein fragment.
 DE Gamma-crystalline; mutant; beta-leaflet; cosmetic; bioseparation;
 KM biosensor; pollution detection; pollution control; gene therapy;
 XX intracellular immunization.
 OS Bos taurus.
 XX
 PN DE19932688-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 13-JUL-1999; 99DE-01032688.
 XX
 PR 13-JUL-1999; 99DE-01032688.
 XX
 PA (FIEDL) FIEDLER U.
 PA (RUDOL) RUDOLPH R.
 XX
 PI Rudolph R, Fiedler U, Boehm G, Reimann C;
 XX
 DR WPI; 2001-148304/16.
 XX
 PT Mutated proteins having beta-leaflet structure and related nucleic acid,
 PT have new or improved properties, e.g. antibody-like specific binding or
 PT catalytic activity.
 XX
 PS Claim 11; Page 16-17; 28pp; German.

XX This invention describes a novel protein (I) with beta-'leaflet'
 CC structure having surface-exposed amino acids, present in at least two
 CC surface-exposed beta-strands of a surface-exposed beta-leaflet. The
 CC protein is altered by targeted mutagenesis so that it has new, or
 CC improved, specific binding, catalytic or fluorescent properties. The
 CC invention also describes (1) DNA (II) that encodes (I); (2) RNA (III)
 CC derived from (II); (3) prokaryotic and eukaryotic vectors and cells that
 CC contain (II) or (III), or their fragments that encode a functional region
 CC of (I); and (4) method for producing (I). (I) are useful for diagnosis
 CC and therapy, in cosmetics, bioseparation and biosensors, and for
 CC pollution detection and control, e.g. for specific targeting of gene
 CC therapy vectors and for intracellular immunization. (I) can be provided
 CC with new or improved specific antibody-like binding, catalytic or
 CC fluorescent properties, without the cost and difficulties associated with
 CC producing complete or recombinant antibodies. (I) are relatively small
 CC (20 kDa) and can be expressed with other components as multifunctional
 CC fusions. They have good stability against low pH, denaturing agents and
 CC high temperatures, conditions under which antibodies are unstable
 CC
 SQ Sequence 198 AA;

Query Match 89.0%; Score 986; DB 4; Length 198;

Best Local Similarity 99.4%; Pred. No. 6.5e-97; Mismatches 0; Gaps 0;

Matches 175; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRIRKEDRGFGHGYSCNSDCPNLOPYFRCNSIRVLSGCMWLYERPNOYQHGYFLRR 60
 DB 6 MGRIRKEDRGFGHGYSCNSDCPNLOPYFRCNSIRVLSGCMWLYERPNOYQHGYFLRR 65
 QY 61 GVPDYQOMMGFNDIRSCLIPQHTGTFMRIRYERDDPFGQSEITDDCPSLQDRPHLT 120
 DB 66 GVPDYQOMMGFNDIRSCLIPQHTGTFMRIRYERDDPFGQSEITDDCPSLQDRPHLT 125
 QY 121 EVHSLNVLGSGWVLYEMPSYRGROYLLRPGYRRLYLDWGAMNAKVSLRRVMDPYS 176
 DB 126 EVHSLNVLGSGWVLYEMPSYRGROYLLRPGYRRLYLDWGAMNAKVSLRRVMDPFA 181

RESULT 4

AA846849
 ID AAB46849 standard; protein; 198 AA.

AC AAB46849;

DT 26-APR-2001 (first entry)

XX Bovine gamma-crystalline protein fragment.

DE Gamma-crystalline; mutant; beta-leaflet; cosmetic; bioseparation;
 KW biosensor; pollution detection; pollution control; gene therapy;
 KM intracellular immunization.

XX Bos taurus.

OS
 PN DE19932688-A1.

PD 18-JAN-2001.

PF 13-JUL-1999; 99DE-01032688.

PR 13-JUL-1999; 99DE-01032688.

XX (FIEDL) FIEDLER U.
 PA (RUDO/) RUDOLPH R.

PI Rudolph R, Fiedler U, Boehm G, Reimann C;

DR WPI; 2001-148304/16.

XX Mutated proteins having beta-leaflet structure and related nucleic acid,
 PT have new or improved properties, e.g. antibody-like specific binding or
 PT catalytic activity.

XX Claim 11; Page 17-18; 28pp; German.

PS This invention describes a novel protein (I) with beta-'leaflet'
 CC structure having surface-exposed amino acids, present in at least two
 CC surface-exposed beta-strands of a surface-exposed beta-leaflet. The
 CC protein is altered by targeted mutagenesis so that it has new, or
 CC improved, specific binding, catalytic or fluorescent properties. The
 CC invention also describes (1) DNA (II) that encodes (I); (2) RNA (III)
 CC derived from (II); (3) prokaryotic and eukaryotic vectors and cells that
 CC contain (II) or (III), or their fragments that encode a functional region
 CC of (I); and (4) method for producing (I). (I) are useful for diagnosis
 CC and therapy, in cosmetics, bioseparation and biosensors, and for
 CC pollution detection and control, e.g. for specific targeting of gene
 CC therapy vectors and for intracellular immunization. (I) can be provided
 CC with new or improved specific antibody-like binding, catalytic or
 CC fluorescent properties, without the cost and difficulties associated with
 CC producing complete or recombinant antibodies. (I) are relatively small
 CC (20 kDa) and can be expressed with other components as multifunctional
 CC fusions. They have good stability against low pH, denaturing agents and
 CC high temperatures, conditions under which antibodies are unstable
 CC
 SQ Sequence 198 AA;

Query Match 85.2%; Score 944; DB 4; Length 198;

Best Local Similarity 95.5%; Pred. No. 2e-92; Mismatches 5; Indels 0; Gaps 0;

Matches 168; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGRIRKEDRGFGHGYSCNSDCPNLOPYFRCNSIRVLSGCMWLYERPNOYQHGYFLRR 60
 DB 6 MGRITVEDRGFGHCYECSSDCPNLOPYFRCNSIRVLSGCMWLYERPNOYQHGYFLRR 65
 QY 61 GVPDYQOMMGFNDIRSCLIPQHTGTFMRIRYERDDPFGQSEITDDCPSLQDRPHLT 120
 DB 66 GVPDYQOMMGFNDIRSCLIPQHTGTFMRIRYERDDPFGQSEITDDCPSLQDRPHLT 125
 QY 121 EVHSLNVLGSGWVLYEMPSYRGROYLLRPGYRRLYLDWGAMNAKVSLRRVMDPYS 176
 DB 126 EVHSLNVLGSGWVLYEMPSYRGROYLLRPGYRRLYLDWGAMNAKVSLRRVMDPFA 181

RESULT 5

ADD47108
 ID ADD47108 standard; protein; 173 AA.

AC ADD47108;

DT 29-JAN-2004 (first entry)

XX Rat Protein P10065, SEQ ID NO 12798.

DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

OS
 PN W02003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Coetigan M;

DR WPI; 2003-268312/26.

XX GENBANK; P10065.

XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1, Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

Sequence 173 AA;

Query Match 69.4%; Score 769.5; DB 7; Length 173;
 Best Local Similarity 77.6%; Pred. No. 7.9e-74;
 Matches 135; Conservative 20; Mismatches 18; Indels 1; Gaps 1;

QY 2 GRIKFKEDRGFGHGYSCNSDCPNLQPYFSRCSIRVLSCGMLYERPNYQHQYFLRG 61
 Db 1 GKITFEYEDRGFGRCYECSSDCPNLQTYFSRCSIRVDSGCMLEYERNYQGYQYFLRG 60
 QY 62 DYPDYQOMMGFNDISIRSCRLIPQHTGTFMRRIYERDDPRGQMSRITDDCPSLQDRFHLTE 121
 Db 61 DYPDYQOMMGFSDISIRSCRSIP-YTSSHRIRLYERDDPRGIVSELTEDCSCIHDFRLNE 119
 QY 122 VHSINVLEGSWVLYEMPSYRGRQYLRLRGYRRLYLDGAMNAKXGSLRRVMDYF 175
 Db 120 IYSMNVLEGSWVLYEMPSYRGRQYLRLRGYRRLYLDGAMNAKXGSLRRVMDYF 173

RESULT 6
 ADE57551
 ID ADE57551 standard; protein; 173 AA.

XX AC ADE57551;
 XX DT 29-JAN-2004 (first entry)
 XX DE Rat Protein P10065, SEQ ID NO 3413.
 XX KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX OS Rattus norvegicus.
 XX PN W02003016475-A2.
 XX PD .27-FEB-2003.
 XX PF 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.

PA (GEMO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M,
 XX WPI; 2003-268312/26.

DR GENBANK; P10065.

PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.

PS Claim 1, Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

Sequence 173 AA;

Query Match 69.4%; Score 769.5; DB 7; Length 173;
 Best Local Similarity 77.6%; Pred. No. 7.9e-74;
 Matches 135; Conservative 20; Mismatches 18; Indels 1; Gaps 1;

QY 2 GRIKFKEDRGFGHGYSCNSDCPNLQPYFSRCSIRVLSCGMLYERPNYQHQYFLRG 61
 Db 1 GKITFEYEDRGFGRCYECSSDCPNLQTYFSRCSIRVDSGCMLEYERNYQGYQYFLRG 60
 QY 62 DYPDYQOMMGFNDISIRSCRLIPQHTGTFMRRIYERDDPRGQMSRITDDCPSLQDRFHLTE 121
 Db 61 DYPDYQOMMGFSDISIRSCRSIP-YTSSHRIRLYERDDPRGIVSELTEDCSCIHDFRLNE 119
 QY 122 VHSINVLEGSWVLYEMPSYRGRQYLRLRGYRRLYLDGAMNAKXGSLRRVMDYF 175
 Db 120 IYSMNVLEGSWVLYEMPSYRGRQYLRLRGYRRLYLDGAMNAKXGSLRRVMDYF 173

RESULT 7
 ADD47114
 ID ADD47114 standard; protein; 173 AA.

XX AC ADD47114;
 XX DT 29-JAN-2004 (first entry)

DE	Rat Protein P10065, SEQ ID NO 12804.	
XX		
KW	Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;	
KW	Chronic constriction injury; CCI, spared nerve injury; SNI; Chung.	
XX		
OS	Rattus norvegicus.	
XX		
PN	WO2003016475-A2.	
XX		
PD	27-FEB-2003.	
XX		
PF	14-AUG-2002; 2002WO-US025765.	
XX		
PR	14-AUG-2001; 2001US-0312147P.	
PR	01-NOV-2001; 2001US-0346382P.	
XX		
PR	26-NOV-2001; 2001US-0333347P.	
XX		
PA	(GENO) GEN HOSPITAL CORP.	
PA	(FARB) BAYER AG.	
P1	WOOLF C, D'URSO D, Befort K, Costigan M;	
XX		
XX	WPI; 2003-268312/26.	
DR	GENBANK; P10065.	
XX		
PS	Claim 1; Page; 1017pp; English.	
XX		
CC	The invention discloses a composition comprising two or more isolated rat	
CC	or human polynucleotides or a polynucleotide which represents a fragment,	
CC	derivative or allelic variation of the nucleic acid sequence. Also	
CC	claimed are a vector comprising the novel polynucleotide, a host cell	
CC	comprising the vector, a method for identifying a nucleotide sequence	
CC	which is differentially regulated in an animal subjected to pain and a	
CC	kit to perform the method, an array, a method for identifying an agent	
CC	that increases or decreases the expression of the polynucleotide sequence	
CC	that is differentially expressed in neuronal tissue of a first animal	
CC	subjected to pain, a method for identifying a compound which regulates	
CC	the expression of a polynucleotide sequence which is differentially	
CC	expressed in an animal subjected to pain, a method for identifying a	
CC	compound that regulates the activity of one or more of the	
CC	polynucleotides, a method for producing a pharmaceutical composition, a	
CC	method for identifying a compound or small molecule that regulates the	
CC	activity in an animal of one or more of the polypeptides given in the	
CC	specification, a method for identifying a compound useful in treating	
CC	pain and a pharmaceutical composition comprising the one or more	
CC	polypeptides or their antibodies. The polynucleotide or the compound that	
CC	modulates its activity is useful for preparing a medicament for treating	
CC	pain (e.g. spinal segmental nerve injury (Chung), chronic constriction	
CC	injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene	
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CC	the specification) which is differentially expressed during pain. Note:	
CC	The sequence data for this patent did not form part of the printed	
CC	specification, but was obtained in electronic form directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences.	
XX		
XX		
SO	Sequence 173 AA;	
QY	Query Match 69.4%; Score 769.5; DB 7; Length 173;	
DB	Beat Local Similarity 77.6%; Pred. No. 7.9e-74;	
	Matches 135; Conservative 20; Mismatches 18; Indels 1; Gaps 1.	
QY	2 GRIKEDRGFGCHYSCNSDCPNLOPFRSRNSIRVLSCGCMLEKRPYQSHOYFLRG 61	
DB	1 GRTIYERGRGFGRCYECGSDCPNLOQTFPSRNSIRVDSGCMLEKRPYQSYQFLRG 60	
QY	62 DYPDYQQMMGFNDSIRSCRLIPQHTGTFMRIRYERDDFGQMSSEITDDCPSLQDRFHLTE 121	
DB	61 DYPDYQQMMGFNDSIRSCRSIP-YTSSHRIRLYERDDYRGVLVSELTEDCSCHDFRLNE 119	
QY	122 VHSLVNLEGSWVLYEMPSYRGQYLLRPGERYRVLDMGAMNAKVGSLRRVDYF 175	

Db 120 IYSHVLEGSVVLVLEMPYRGRQTLRLRGDYRRHYDGMAMAKVSLRRVMDLY 173

RESULT 8
ADD47112
ID ADD47112 standard; protein; 173 AA.
XX ADD47112;
AC
AD 29-JAN-2004 (first entry)
DT
XX
XX
DE Rat Protein AAA40981, SEQ ID NO 12802.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SN1; Chung.
XX
XX Rattus norvegicus.
OS
XX
XX WO2003016475-A2.
PN
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX WOOLF C, D'URSO D, Befort K, Costigan M;
P1
XX MPI; 2003-268312/26.
DR GENBANK; AAA40981.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat
or human polynucleotides or a polynucleotide which represents a fragment,
derivative or allelic variation of the nucleic acid sequence. Also
claimed are a vector comprising the novel polynucleotide, a host cell
comprising the vector, a method for identifying a nucleotide sequence
which is differentially regulated in an animal subjected to pain and a
kit to perform the method, an array, a method for identifying an agent
that increases or decreases the expression of the polynucleotide sequence
that is differentially expressed in neuronal tissue of a first animal
subjected to pain, a method for identifying a compound which regulates
the expression of a polynucleotide sequence which is differentially
expressed in an animal subjected to pain, a method for identifying a
compound that regulates the activity of one or more of the
polynucleotides, a method for producing a pharmaceutical composition, a
method for identifying a compound or small molecule that regulates the
activity in an animal of one or more of the polypeptides given in the
specification, a method for identifying a compound useful in treating
pain and a pharmaceutical composition comprising the one or more
polypeptides or their antibodies. The polynucleotide or the compound that
modulates its activity is useful for preparing a medicament for treating
pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
injury (CCI) and spared nerve injury (SN1) in an animal (e.g. gene
therapy). The sequence presented is a rat protein (shown in Table 2 of
the specification) which is differentially expressed during pain. Note:
The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic form directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

Sequence 173 AA;

Query Match 69.4%; Score 769.5; DB 7; Length 173;

Best Local Similarity 77.6%; Pred. No. 7,9e-74;
Matches 135; Conservative 20; Mismatches 18; Indels 1; Gaps 1;

QY 2 GRIKFKEDRGFGQGHYHSCNDCPNLOPYFRCNSIRVLSGCMWLYRPNYQGHQYFLRRG 61
DB 1 GKITFFEDRGFGQRCYECSSDCPNLOPYFRCNSIRVDSGCMWLYRPNYQGHQYFLRRG 60

QY 62 DYDPYQOMWGFNDISIRCLIPQHTGTFMRRIYERDDFRGOMSEITDDCPSLQDRPHLITE 121
DB 61 DYDPYQOMWGFNDISIRCLIP-QYTSNHRIRLYERDDYRGLVSELTEDSCCHDRRLNE 119

QY 122 VHSJLVLEGSWVLYEMPNYRGRQYLLRPGERYRRLDWMGAMNAKVGSIRVMDPY 175
DB 120 IYSMHVLEGSWVLYEMPNYRGRQYLLRPGDYRRYHDWGMADAKVGSIRVMDLY 173

RESULT 9
ADD47118
ID ADD47118 standard; protein; 173 AA.

AC ADD47118;
DT 29-JAN-2004 (first entry)

DE Rat Protein AAA40981, SEQ ID NO 12808.

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

OS Rattus norvegicus.

XX MO2003016475-A2.
XX 27-FEB-2003.

PF 14-AUG-2002; 2002MO-US025765.
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.

PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;
DR WPI; 2003-268312/26.
DR GENBANK; AAA40981.

PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

PS Claim 1; Page: 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that

CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 173 AA;

QY 69.4%; Score 769.5; DB 7; Length 173;
Best Local Similarity 77.6%; Pred. No. 7,9e-74;
Matches 135; Conservative 20; Mismatches 18; Indels 1; Gaps 1;

QY 2 GRIKFKEDRGFGQGHYHSCNDCPNLOPYFRCNSIRVLSGCMWLYRPNYQGHQYFLRRG 61
DB 1 GKITFFEDRGFGQRCYECSSDCPNLOPYFRCNSIRVDSGCMWLYRPNYQGHQYFLRRG 60

QY 62 DYDPYQOMWGFNDISIRCLIPQHTGTFMRRIYERDDFRGOMSEITDDCPSLQDRPHLITE 121
DB 61 DYDPYQOMWGFNDISIRCLIP-QYTSNHRIRLYERDDYRGLVSELTEDSCCHDRRLNE 119

QY 122 VHSJLVLEGSWVLYEMPNYRGRQYLLRPGERYRRLDWMGAMNAKVGSIRVMDPY 175
DB 120 IYSMHVLEGSWVLYEMPNYRGRQYLLRPGDYRRYHDWGMADAKVGSIRVMDLY 173

RESULT 10
ADE83335
ID ADE83335 standard; protein; 173 AA.

AC ADE83335;
DT 29-JAN-2004 (first entry)

DE Rat Protein P10065, SEQ ID NO 10928.

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

OS Rattus norvegicus.

XX MO2003016475-A2.
XX 27-FEB-2003.

PF 14-AUG-2002; 2002MO-US025765.
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.

PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;
DR WPI; 2003-268312/26.
DR GENBANK; P10065.

PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

PS Claim 1; Page: 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 173 AA;
Query Match 69.4%; Score 769.5; DB 7; Length 173;
Best Local Similarity 77.6%; Pred. No. 7.9e-74;
Matches 135; Conservative 20; Mismatches 18; Indels 1; Gaps 1;
QY 2 GRIKFKEDRGFGHGYSCNSDCPNLQPYFSRNSIRVLSGCMLYERPNOYGHQYFLRRG 61
DB 1 GKIRFYEDRGFGHGYSCNSDCPNLQPYFSRNSIRVDSGCMLYERPNOYGYFLRRG 60
QY 62 DYPPYQGMGFNSIRSCRLIPQHTGTFRRRIYERDPRGMSITDDCSLQRFHLTE 121
DB 61 DYPPYQGMGFNSIRSCRSIP-YTSSHRIRLYERDPRGIVSRLTEDCSCIHFRFRINE 119
QY 122 VHSINLVLEGSWVLYEMPSYRGROYLLRGEYRRLYLDGAMNAAKGSLLRWVDFY 175
DB 120 IYSMHVLEGSWVLYEMPSYRGROYLLRGGDYRRYHDGAMDAKGSLLRWVDFY 173
RESULT 11
ADE57555 standard; protein; 173 AA.
XX
AC ADE57555;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein AAA40981, SEQ ID NO 3417.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PE 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
XX
PR 01-NOV-2001; 2001US-0346382P.
XX
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PA (PARB) BAYER AG.
XX
PI WOOLF C, D'URSO D, Befort K, Costigan M,
XX
XX WPI; 2003-268312/26.
XX
XX GENBANK; AAA40981.
XX

PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 173 AA;
Query Match 69.4%; Score 769.5; DB 7; Length 173;
Best Local Similarity 77.6%; Pred. No. 7.9e-74;
Matches 135; Conservative 20; Mismatches 18; Indels 1; Gaps 1;
QY 2 GRIKFKEDRGFGHGYSCNSDCPNLQPYFSRNSIRVLSGCMLYERPNOYGHQYFLRRG 61
DB 1 GKIRFYEDRGFGHGYSCNSDCPNLQPYFSRNSIRVDSGCMLYERPNOYGYFLRRG 60
QY 62 DYPPYQGMGFNSIRSCRLIPQHTGTFRRRIYERDPRGMSITDDCSLQRFHLTE 121
DB 61 DYPPYQGMGFNSIRSCRSIP-YTSSHRIRLYERDPRGIVSRLTEDCSCIHFRFRINE 119
QY 122 VHSINLVLEGSWVLYEMPSYRGROYLLRGEYRRLYLDGAMNAAKGSLLRWVDFY 175
DB 120 IYSMHVLEGSWVLYEMPSYRGROYLLRGGDYRRYHDGAMDAKGSLLRWVDFY 173
RESULT 12
ADD47104 standard; protein; 173 AA.
XX
AC ADD47104;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein AAA40988, SEQ ID NO 12794.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PE 14-AUG-2002; 2002WO-US025765.
XX

14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEBO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
DR WPI; 2003-268312/26.
DR GENBANK; AAA40388.
XX
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 173 AA;
SQ
Query Match 68.4%; Score 757.5; DB 7; Length 173;
Best Local Similarity 75.3%; Pred. No. 1.5e-72;
Matches 131; Conservative 22; Mismatches 20; Indels 1; Gaps 1;
QY 2 GRIFKEDRGFGHGYSCNSDCEPILQPFSCRNSIRVLSCGMLYERPNOHQYFLRRG 61
DB 1 GKIFTEYEDRGFGHGYSCNSDCEPILQPFSCRNSIRVLSCGMLYERPNOHQYFLRRG 60
QY 62 DYPIYQOMMGFNDSIRSCRLIPQHTGFRMRIRYERDDPFGOMSEITDDCSLQDRPHLT 121
DB 61 DYPIYQOMMGFNDSIRSCRLIPQHTGFRMRIRYERDDPFGOMSEITDDCSLQDRPHLT 119
QY 122 VHSILNVLGSGWLVLYEMPSYRGRQYLRLPGERYRRLDGMANNAKVGSLRRVMDP 175
DB 120 FHSFHVIEGWWLVLYEMPSYRGRQYLRLPGERYRRLDGMANNAKVGSLRRVMDP 173
RESULT 13
ABG21006
ID ABG21006 standard; protein; 174 AA.
XX
XX ABG21006;
XX
XX 18-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #20997.
DE

XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW Food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
OS
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX N-PSDB; AAS85193.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID NO 51365; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences. The sequence presented is a rat protein (shown in
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 174 AA;
SQ
Query Match 65.7%; Score 727.5; DB 4; Length 174;
Best Local Similarity 73.6%; Pred. No. 2.5e-69;
Matches 128; Conservative 20; Mismatches 25; Indels 1; Gaps 1;
QY 1 MGRIFKEDRGFGHGYSCNSDCEPILQPFSCRNSIRVLSCGMLYERPNOHQYFLRR 60
DB 1 MKITLYEDRGFGHGYSCNSDCEPILQPFSCRNSIRVLSCGMLYERPNOHQYFLRR 60
QY 61 GDYPIYQOMMGFNDSIRSCRLIPQHTGFRMRIRYERDDPFGOMSEITDDCSLQDRPHLT 120
DB 61 GDYADHQOMMGLSIVSVSCRILP-HSSGSHRIRIYEREDYRQOMSEITDDCSLQDRPHLT 119
QY 121 EVHSILNVLGSGWLVLYEMPSYRGRQYLRLPGERYRRLDGMANNAKVGSLRRVMDP 174
DB 120 EHSILNVLGSGWLVLYEMPSYRGRQYLRLPGERYRRLDGMANNAKVGSLRRVMDP 173
RESULT 14
ADD47106
ID ADD47106 standard; protein; 174 AA.
DE

XX AC ADD47106;
 XX XX 29-JAN-2004 (first entry)
 XX DE Human Protein NP_008822, SEQ ID NO 12796.
 XX XX Human; pain; neuronal tissue; gene therapy;
 KM spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX OS Homo sapiens.
 XX PN WO2003016475-A2.
 XX PD 27-FEB-2003.
 XX PF 14-AUG-2002; 2002WO-US025765.
 XX PR 14-AUG-2001; 2001US-0312147P.
 XX PR 01-NOV-2001; 2001US-0346382P.
 XX PR 26-NOV-2001; 2001US-033347P.
 XX PA (GENO) GEN HOSPITAL CORP.
 XX PA (FARB) BAYER AG.
 XX PI Woolf C, D'urao D, Befort K, Coatsigan M,
 XX DR WPI; 2003-268312/26.
 XX DR GENBANK; NP_008822.
 XX PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX PS Claim 1; Page; 1017P; English.
 XX XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX XX Sequence 174 AA;
 SQ

Query Match 65.7%; Score 727.5; DB 7; Length 174;
 Best Local Similarity 73.6%; Pred. No. 2.5e-65;
 Matches 128; Conservative 20; Mismatches 25; Indels 1; Gaps 1;
 1 MGRIFKEDRGFOGHYSCNSDCPNLOPYPSPRCNSINVLSCWMLYERPNYOGHGYFLRR 60
 1 MGRITLVEDRGFOGRHNEGCSHDHNLQPIYSRCHSNAVDGCMWLYQPNYSGIQYFLRR 60
 Db

Qy 61 GGVDPDYQOMMGFNDISIRSCRLIPQHTGTFMRIRYERDDFRGOMSEITDPCSLQDRFHLT 120
 Db 61 GGVADHQOMMGJSDSVRSCLLP-HSGSHIRIRLYEREDYRGQITETEDSCIQDFFRN 119
 Qy 121 EVHSLNVLGSGWLVYEMPSYRGROYLLRPGEYRYLLMGANAKVGLRVMDP 174
 Db 120 EIHSLNVLGSGWLVYELSNYRGQYLLMPGDRYRGQWKATNARVGLSRVIDF 173
 RESULT 15
 ID ADCJ1213 standard; protein; 362 AA.
 XX AC ADCJ1213;
 XX XX 18-DEC-2003 (first entry)
 XX DE Human novel polypeptide sequence, SEQ ID NO:1295.
 XX KW Human; diagnostic; drug screening; forensics; gene mapping;
 KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;
 KW neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
 KW ulcers; osteoporosis; autoimmune disease; cancer;
 KW molecular weight marker; food supplement; antiparkinsonian; nootropic;
 KW neuroprotective; antinaemic; anticoagulant; thrombolytic; vulnerrary;
 KW antitumor; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
 KW gene therapy; chromosome 18.
 XX OS Homo sapiens.
 XX PN WO2003029271-A2.
 XX PD 10-APR-2003.
 XX PF 24-SEP-2002; 2002WO-US030474.
 XX PR 24-SEP-2001; 2001US-0324631P.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
 PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
 PI Haley-Vicente D, Dramanac RT;
 XX DR WPI; 2003-371981/35.
 XX DR N-PSTB; ADCJ0242.
 XX PT New polynucleotide and polypeptide useful for diagnosing, preventing or
 PT treating conditions such as neurodegenerative diseases, anemias, platelet
 PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
 PT cancer.
 XX PS Claim 20; SEQ ID NO 1295; 1185P; English.
 XX XX The invention relates to 971 novel human cDNA sequences (ADC29919-
 CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
 CC invention also relates to nucleic acid sequences over 99% identical with
 CC the novel human cDNAs. The invention additionally encompasses expression
 CC vectors and host cells comprising a nucleic acid of the invention; the
 CC recombinant production of a polypeptide of the invention; an antibody
 CC against a polypeptide of the invention; a method of detecting
 CC polynucleotides or polypeptides of the invention; and methods of
 CC identifying a compound which binds to a polypeptide of the invention. The
 CC invention further discloses methods of preventing, treating or
 CC ameliorating a medical condition; kits comprising polynucleotide probes
 CC and/or monoclonal antibodies for carrying out the methods of the
 CC invention; methods for the identification of compounds that modulate the
 CC expression or activity of the polynucleotide and/or polypeptide; and 767
 CC contig sequences corresponding to the cDNA sequences by the contigs (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628-ADC33394). The nucleic acids and polypeptides of the invention are
 CC useful in diagnostics, drug screening, forensics, gene mapping, in the

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2005, 12:03:35 ; Search time 16 Seconds

(without alignments)
1184,669 Million cell updates/sec

Title: US-10-030-605A-21

Perfect score: 1108
Sequence: 1 MGRKFKEDKFGQGHYSCN.....PNSSVDKLAALAEHHHHH 197Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	943	85.1	175	1	gamma-crystallin I
2	881	79.5	175	2	B24060 gamma-crystallin 1
3	864	78.0	175	1	CYMSG3 gamma-B-crystallin
4	830	74.9	175	1	CYHUG1 gamma-crystallin 1
5	783.5	70.7	174	2	D24060 gamma-crystallin 2
6	778.5	70.3	174	1	CYMSG2 gamma-crystallin 2
7	778.5	70.3	174	2	I63432 gamma-crystallin 2
8	775.5	70.0	174	2	C24060 gamma-crystallin 2
9	774.5	69.9	174	2	A24060 gamma-crystallin 1
10	773.5	69.8	173	1	CYRUC1 gamma-crystallin 1
11	770.5	69.5	174	2	S04266 gamma-crystallin 1
12	770.5	69.5	174	1	CYMSG1 gamma-crystallin 1
13	767.5	69.3	174	2	J50596 gamma-E-crystallin 4
14	765.5	69.1	174	1	CYMSG4 gamma-crystallin 4
15	764.5	69.0	174	2	B26811 gamma-E-crystallin 4
16	762.5	68.8	174	2	B24060 gamma-crystallin 4
17	762.5	68.8	174	2	I45881 gamma-C-crystallin
18	756.5	68.3	174	2	S33526 gamma-crystallin 2
19	752.5	67.9	174	1	CYRUC2 gamma-crystallin 2
20	740.5	66.8	170	1	CYRUC2 gamma-crystallin 2
21	726.5	65.6	174	1	CYHUG2 gamma-D-crystallin 5
22	723.5	65.3	174	2	I77413 gamma-crystallin 5
23	713.5	64.6	174	2	B26955 gamma-crystallin 5
24	686	61.9	176	2	S45015 gamma-F-crystallin M
25	684.5	61.8	159	2	I49618 gamma-C-crystallin
26	682.5	61.6	151	2	S45016 gamma-crystallin S
27	656	59.2	173	2	S45016 gamma-crystallin S
28	645	58.2	175	2	UN0682 gamma3-crystallin

30	639	57.7	168	1	CYFG32 gamma-crystallin I
31	639	57.7	169	2	T01783 gamma2-crystallin
32	631	56.9	176	2	JN0681 gamma2-crystallin
33	627	56.6	177	2	S52842 gamma-M1-crystal
34	621	56.0	175	2	UN0680 gamma1-crystallin
35	616	55.6	177	2	S52843 gamma-M1-2 crystal
36	613	55.3	172	2	PN0545 gamma4-crystallin
37	610	55.1	173	2	S45017 gamma-crystallin S
38	561	50.6	133	1	CYFG5 gamma-crystallin I
39	554.5	50.0	174	2	S07146 gamma-B-crystallin
40	545.5	49.2	174	2	S18460 gamma-crystallin m
41	543.5	49.1	177	2	JC2357 gamma-crystallin m
42	538	48.6	173	1	CYCA62 gamma-crystallin m
43	537.5	48.5	178	1	CYBOS gamma-s-crystallin
44	532.5	48.1	178	1	S10601 gamma-crystallin M
45	531.5	48.0	175	2	JC2354 gamma-crystallin M

ALIGNMENTS

RESULT 1

CYBOG gamma-crystallin II - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 28-Feb-1986 #sequence revision 03-Feb-1994 #text change 09-Jul-2004

C:Accession: A29655; A02928; A50263; A60890; A60815; A02529; S04265

R:Hay, R.E.; Woods, W.D.; Church, R.L.; Petrash, J.M.
Biochem. Biophys. Res. Commun. 146, 332-338, 1987

A:Title: cDNA clones encoding bovine gamma-crystallins.

A:Reference number: A90133; MUID:87270760; PMID:3606621

A:Accession: A29655

A:Molecule type: mRNA

A:Residues: 1-175 <HA>

A:Cross-references: UNIPROT:P02526; GB:M16894; NID:G162918; PIDN:AAA30476.1; PID:G162919

R:Bhat, S.P.; Spector, A.

DNA 3, 287-295, 1984

A:Title: Complete nucleotide sequence of a cDNA derived from calf lens gamma-crystallin

A:Reference number: A02928; MUID:85026663; PMID:6052016

A:Accession: A02928

A:Molecule type: mRNA

A:Residues: 2-119, 'S', '121-175

A:Cross-references: GB:X01036; NID:G162916; PIDN:AAA30475.1; PID:G162917

A:Reference number: A90263; MUID:73054483; PMID:4674126

A:Accession: A90263

A:Molecule type: protein

A:Residues: 2-17, 'Q', '19-21, 'NN', '23, 'LOP', '28-39, 'VHSL', '45-46, 'MLQ', '48-49, 'D', '51, '53-54, '56, 'A>Note: Portions of this sequence were assigned by composition rather than by direct seq

R:Chou, S.H.; Azari, P.; Himel, M.E.

J. Protein Chem. 7, 67-80, 1988

A:Title: Physicochemical characterization of gamma-crystallins from bovine lens-hydrodyn.

A:Reference number: A60890; MUID:89351571; PMID:3255364

A:Accession: A60890

A:Molecule type: protein

A:Residues: 2-26 <CHI>

R:McMurtrei, M.J.; Gawinowicz-Kolke, M.A.; Chiesa, R.; Spector, A.

Arch. Biochem. Biophys. 262, 609-619, 1988

A:Title: The disulfide content of calf gamma-crystallin.

A:Reference number: A60815; MUID:86208422; PMID:3364984

A:Accession: A60815

A:Molecule type: protein

A:Residues: 2-26 <MCD>

R:Blundell, T.; Lindley, P.; Miller, L.; Mose, D.; Slingsby, C.; Tickle, I.; Turnell, B.
Nature 289, 771-777, 1981
A:Title: The molecular structure and stability of the eye lens: x-ray analysis of gamma-cr
A:Reference number: A93247; MUID:81123111; PMID:7454942
A:Contents: annotation; X-ray crystallography, 2.6 angstroms
J.White, H.E.; Driessen, H.P.C.; Slingsby, C.; Mose, D.S.; Lindley, P.F.
J. Mol. Biol. 207, 217-235, 1989

A>Title: Packing interactions in the eye-lens. Structural analysis. internal symmetry an
 A:Reference number: S04265; MUID:89233855; PMID:2738925
 A:Contents: annotation
 C:Comment: The protein has a two-domain beta-structure, folded into four very similar G
 C:Superfamily: beta-crystallin
 C:Keywords: duplication; eye lens
 F:2-40/Domain: crystallin repeat <GK1>
 F:41-83/Domain: crystallin repeat <GK2>
 F:89-129/Domain: crystallin repeat <GK3>
 F:130-169/Domain: crystallin repeat <GK4>

Query Match 85.1%; Score 943; DB 1; Length 175;
 Best Local Similarity 96.0%; Pred. No. 8.8e-82;
 Matches 168; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MGRIRKEDRGFGHGYSCNSDCPNLQPFSSCNSTRVLSGCMWLYERPNNQGHQYFLRR 60
 DB 1 MGRITFEDRGFGHGYECSSDCPNLQPFSSCNSTRVDSGCMWLYERPNNQGHQYFLRR 60
 QY 61 GDYPDYQOMMGFNDSIRSCRLIPQHTGFRMRIRYERDDPRGQMSSETDDCPSLQDRFHLT 120
 DB 61 GDYPDYQOMMGFNDSIRSCRLIPQHTGFRMRIRYERDDPRGQMSSETDDCPSLQDRFHLT 120
 QY 121 EVHSLNVLEGSWVLYEMPSYRGRQYLRLRGEYRRLYLDGMANNAKVGLRRVMDFY 175
 DB 121 EVHSLNVLEGSWVLYEMPSYRGRQYLRLRGEYRRLYLDGMANNAKVGLRRVMDFY 175

RESULT 2

gamma-crystallin 1-2 - rat
 N:Alternate names: gamma-B-crystallin
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
 C:Accession: B24060; MUID:183431
 R:Den Dunnen, J.T.; Moormann, R.J.M.; Lubben, N.H.; Schoenmakers, J.G.G.
 J.Mol. Biol. 189, 37-46, 1986
 A>Title: Concetred and divergent evolution within the rat gamma-crystallin gene family.
 A:Reference number: A92927; MUID:87060933; PMID:3783678
 A:Accession: B24060
 A:Molecule type: DNA
 A:Residues: 1-175 <DNS>
 A:Cross-references: UNIPROT:P10066; GB:M19359; NID:g203626; PIDN:AAA40982.1; PID:g203628
 R:Den Dunnen, J.T.; van Neck, J.W.; Cremers, F.P.M.; Lubben, N.H.; Schoenmakers, J.G.G.
 Gene 78, 201-213, 1989
 A>Title: Nucleotide sequence of the rat gamma-crystallin gene region and comparison with
 A:Reference number: I60312; MUID:89378747; PMID:2777080
 A:Accession: I83431
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-175 <RES>
 A:Cross-references: GB:M19359; NID:g203626; PIDN:AAA40982.1; PID:g203628
 C:Genetics:
 A:Introns: 3/3; 84/3
 C:Superfamily: beta-crystallin
 C:Keywords: duplication

Query Match 79.5%; Score 881; DB 2; Length 175;
 Best Local Similarity 88.6%; Pred. No. 6.3e-76;
 Matches 155; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 MGRIRKEDRGFGHGYSCNSDCPNLQPFSSCNSTRVLSGCMWLYERPNNQGHQYFLRR 60
 DB 1 MGRITFEDRGFGHGYECSSDCPNLQPFSSCNSTRVDSGCMWLYERPNNQGHQYFLRR 60
 QY 61 GDYPDYQOMMGFNDSIRSCRLIPQHTGFRMRIRYERDDPRGQMSSETDDCPSLQDRFHLT 120
 DB 61 GDYPDYQOMMGFNDSIRSCRLIPQHTGFRMRIRYERDDPRGQMSSETDDCPSLQDRFHLT 120
 QY 121 EVHSLNVLEGSWVLYEMPSYRGRQYLRLRGEYRRLYLDGMANNAKVGLRRVMDFY 175
 DB 121 EVHSLNVLEGSWVLYEMPSYRGRQYLRLRGEYRRLYLDGMANNAKVGLRRVMDFY 175

RESULT 3

gamma-B-crystallin - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Mar-1987 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
 C:Accession: I48359; A02933; S33523
 R:Graw, J.; Liebschein, A.; Pleterowski, D.; Schmitt-John, T.; Werner, T.
 Gene 136, 145-156, 1993
 A>Title: Genomic sequences of murine gamma B- and gamma C-crystallin-encoding genes: prom
 A:Reference number: I48359; MUID:94123992; PMID:8233998
 A:Accession: I48359
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-175 <RES>
 A:Cross-references: UNIPROT:P04344; EMBL:Z22573; NID:g311633; PIDN:CAA80296.1; PID:g3116
 R:Beltman, M.L.; Lok, S.; Wisnow, G.; Platisorsky, J.; Trecon, J.A.; Gold, R.J.M.; Tsui,
 Proc. Natl. Acad. Sci. U.S.A. 81, 7762-7766, 1984
 A>Title: gamma-crystallin family of the mouse lens: structural and evolutionary relations
 A:Reference number: A94021; MUID:85088487; PMID:6096855
 A:Accession: A02933
 A:Molecule type: mRNA
 A:Residues: 41-150, 'M', 152-175

 A:Comment: There are at least seven different gamma crystallins identified in mouse lens
 C:Genetics:
 A:Introns: 3/3; 84/3
 C:Superfamily: beta-crystallin
 C:Keywords: duplication; eye lens
 F:2-40/Domain: crystallin repeat <GK1>
 F:41-83/Domain: crystallin repeat <GK2>
 F:89-129/Domain: crystallin repeat <GK3>
 F:130-169/Domain: crystallin repeat <GK4>

Query Match 78.0%; Score 864; DB 1; Length 175;
 Best Local Similarity 86.3%; Pred. No. 2.5e-74;
 Matches 151; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 MGRIRKEDRGFGHGYSCNSDCPNLQPFSSCNSTRVLSGCMWLYERPNNQGHQYFLRR 60
 DB 1 MGRITFEDRSFGRCYECSSDCPNLQYFSRCNSVRVDSGCMWLYERPNNQGHQYFLRR 60
 QY 61 GDYPDYQOMMGFNDSIRSCRLIPQHTGFRMRIRYERDDPRGQMSSETDDCPSLQDRFHLT 120
 DB 61 GEYPDYQOMMGFNDSIRSCRLIPQHTGFRMRIRYERDDPRGQMSSETDDCPSLQDRFHLT 120
 QY 121 EVHSLNVLEGSWVLYEMPSYRGRQYLRLRGEYRRLYLDGMANNAKVGLRRVMDFY 175
 DB 121 EVHSLNVLEGSWVLYEMPSYRGRQYLRLRGEYRRLYLDGMANNAKVGLRRVMDFY 175

RESULT 4

gamma-crystallin 1-2 - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
 C:Accession: A24520
 R:Den Dunnen, J.T.; Moormann, R.J.M.; Cremers, F.P.M.; Schoenmakers, J.G.G.
 Gene 38, 197-204, 1985
 A>Title: Two human gamma-crystallin genes are linked and riddled with Alu-repeats.
 A:Reference number: A91536; MUID:86056977; PMID:4065573
 A:Accession: A24520
 A:Molecule type: DNA
 A:Residues: 1-175 <DNS>
 A:Cross-references: UNIPROT:P07316; GB:M11971; NID:g181114; PIDN:AAA52113.1; PID:g181118
 C:Genetics:
 A:Gene: GDB:CRYGA; CRYG1
 A:Cross-references: GDB:119076; OMIM:123660
 A:Map position: 2q33-2q35
 A:Introns: 3/3; 84/3
 C:Superfamily: beta-crystallin
 C:Keywords: duplication; eye lens
 F:2-15/Product: gamma-crystallin 1-2 #status predicted <MPT>

F:2-40/Domain: crystalin repeat <GK1>
 F:41-83/Domain: crystalin repeat <GK2>
 F:89-129/Domain: crystalin repeat <GK3>
 F:130-169/Domain: crystalin repeat <GK4>

Query Match 74.9%; Score 830; DB 1; Length 175;
 Best Local Similarity 81.7%; Pred. No. 4,2e-71;
 Matches 143; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 MGRIFKEDRGFOGHYSCNSDCPNLOPYFSRCNSIRVLSGCMWLYERPNOGHQYFLRR 60
 DB 1 MGRITFYEDRAFOGRSECTDPCPNLOPYFSRCNSIRVLSGCMWLYERPNOGHQYFLRR 60
 QY 61 GDYVDYQOQMGFNDISIRSCRLIPQHTGTFMRIRYERDDFRGQSEITDDCPSLQDRPHLT 120
 DB 61 GEXYVDYQOQMGFNDISIRSCRLIPQHTGTFMRIRYERDDFRGQSEITDDCPSLQDRPHLT 120
 QY 121 EVHSLNVLGSGWVLYEMPYRGRQYLLRPGERYRRYLDGMANNAKVGSLRRVMDPY 175
 DB 121 EHSNVLGSGWVLYEMPYRGRQYLLRPGERYRRYLDGMANNAKVGSLRRVMDPY 175

RESULT 5
 D24060
 gamma-crystallin 2-2 - rat

N/Alternate names: gamma-D-crystallin
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
 C/Accession: D24060; I83433; S60744
 R/den Dunnen, J.T.; Moormann, R.J.M.; Lubben, N.H.; Schoenmakers, J.G.G.
 J. Mol. Biol. 189, 37-46, 1986
 A/Title: Concerted and divergent evolution within the rat gamma-crystallin gene family.
 A/Reference number: A92927; MUID:87060933; PMID:3783678
 A/Accession: D24060

A/Molecule type: DNA
 A/Residues: 1-174 <DNS>
 A/Cross-references: UNIPROT:P10067; GB:M19359; NID:g203626; PIDN:AAA40984.1; PID:g203630
 R/den Dunnen, J.T.; van Neck, J.W.; Cremers, F.P.M.; Lubben, N.H.; Schoenmakers, J.G.G.
 Gene 78, 201-213, 1989
 A/Title: Nucleotide sequence of the rat gamma-crystallin gene region and comparison with
 A/Reference number: I60312; MUID:89378747; PMID:2777080
 A/Accession: I83433

A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-174 <RES>
 A/Cross-references: GB:M19359; NID:g203626; PIDN:AAA40984.1; PID:g203630
 R/Ooki, K.; Amuro, N.; Shimizu, Y.; Okazaki, T.
 Biochimie 76, 398-403, 1994
 A/Title: High level expression of rat gamma-D-crystallin in Escherichia coli.
 A/Reference number: S60744; MUID:95151850; PMID:7849105

A/Accession: S60744
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-174 <OOK>
 A/Cross-references: EMBL:X57169; NID:g929827; PIDN:CAA40458.1; PID:g929828
 C/Genetics: 3/3; 84/3
 A/Intons: 3/3; 84/3
 C/Superfamily: beta-crystallin
 C/Keywords: duplication

Query Match 70.7%; Score 783.5; DB 2; Length 174;
 Best Local Similarity 78.3%; Pred. No. 1e-66;
 Matches 137; Conservative 19; Mismatches 18; Indels 1; Gaps 1;

QY 1 MGRIFKEDRGFOGHYSCNSDCPNLOPYFSRCNSIRVLSGCMWLYERPNOGHQYFLRR 60
 DB 1 MGRITFYEDRAFOGRSECTDPCPNLOPYFSRCNSIRVLSGCMWLYERPNOGHQYFLRR 60
 QY 61 GDYVDYQOQMGFNDISIRSCRLIPQHTGTFMRIRYERDDFRGQSEITDDCPSLQDRPHLT 120
 DB 61 GDYVDYQOQMGFNDISIRSCRLIP-HAGSHRIRLYERDDFRGQSEITDDCPSLQDRPHLT 119
 QY 121 EVHSLNVLGSGWVLYEMPYRGRQYLLRPGERYRRYLDGMANNAKVGSLRRVMDPY 175

DB 120 EHSNVLGSGWVLYEMPYRGRQYLLRPGERYRRYLDGMANNAKVGSLRRVMDPY 174

RESULT 6

CYMSG2
 gamma-crystallin 2 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004

C/Accession: A02931
 R/Breitman, M.L.; Lok, S.; Wistow, G.; Platiogorsky, J.; Treton, J.A.; Gold, R.J.M.; Tsui
 Proc. Natl. Acad. Sci. U.S.A. 81, 7762-7766, 1984
 A/Title: gamma-crystallin family of the mouse lens: structural and evolutionary relations;
 A/Reference number: A94021; MUID:85088487; PMID:6096855

A/Accession: A02931
 A/Molecule type: mRNA
 A/Residues: 1-174 <BRE>
 A/Cross-references: UNIPROT:P02528; GB:X02584; NID:g192786; PIDN:AAA03228.1; PID:g309198
 C/Comment: There are at least seven different gamma crystallins identified in mouse lens
 C/Superfamily: beta-crystallin
 C/Keywords: duplication; eye lens

F:2-40/Domain: crystalin repeat <GK1>
 F:41-83/Domain: crystalin repeat <GK2>
 F:88-128/Domain: crystalin repeat <GK3>
 F:129-168/Domain: crystalin repeat <GK4>

Query Match 70.3%; Score 778.5; DB 1; Length 174;
 Best Local Similarity 77.1%; Pred. No. 3e-66;
 Matches 135; Conservative 21; Mismatches 18; Indels 1; Gaps 1;

QY 1 MGRIFKEDRGFOGHYSCNSDCPNLOPYFSRCNSIRVLSGCMWLYERPNOGHQYFLRR 60
 DB 1 MGRITFYEDRAFOGRSECTDPCPNLOPYFSRCNSIRVLSGCMWLYERPNOGHQYFLRR 60
 QY 61 GDYVDYQOQMGFNDISIRSCRLIPQHTGTFMRIRYERDDFRGQSEITDDCPSLQDRPHLT 120
 DB 61 GDYVDYQOQMGFNDISIRSCRLIP-HSSSHRIRLYERDDFRGQSEITDDCPSLQDRPHLT 119
 QY 121 EVHSLNVLGSGWVLYEMPYRGRQYLLRPGERYRRYLDGMANNAKVGSLRRVMDPY 175
 DB 121 DFHSFVMEGYSWVLYEMPYRGRQYLLRPGERYRRYLDGMANNAKVGSLRRVMDPY 174

RESULT 7

gamma-crystallin - rat
 N/Alternate names: gamma-E-crystallin
 C/Species: Rattus norvegicus (Norway rat)

C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C/Accession: I56381; I83434
 R/Moormann, R.J.; den Dunnen, J.T.; Mulleners, L.; Andreoli, P.; Bloemendal, H.; Schoenme
 J. Mol. Biol. 171, 353-368, 1993
 A/Title: Strict co-linearity of genetic and protein folding domains in an intragenic
 A/Reference number: I56381; MUID:84114867; PMID:6319707

A/Accession: I56381
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-174 <RES>
 A/Cross-references: UNIPROT:P02528; EMBL:X00271; NID:g56193; PIDN:CAA5073.1; PID:g29591
 R/den Dunnen, J.T.; van Neck, J.W.; Cremers, F.P.M.; Lubben, N.H.; Schoenmakers, J.G.G.
 Gene 78, 201-213, 1989
 A/Title: Nucleotide sequence of the rat gamma-crystallin gene region and comparison with
 A/Reference number: I60312; MUID:89378747; PMID:2777080

A/Accession: I83434
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-174 <RE2>
 A/Cross-references: GB:M19359; NID:g203626; PIDN:AAA40985.1; PID:g203631
 C/Genetics: 3/3; 84/3
 A/Intons: 3/3; 84/3
 C/Superfamily: beta-crystallin
 C/Keywords: duplication

RESULT 15

CYMSG4

gamma-crystallin 4 - mouse

C/Species: Mus musculus (house mouse)

C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004

C/Accession: A02935; I49613

R/Breiman, M.L.; Lok, S.; Wistow, G.; Platigorsky, J.; Treton, J.A.; Gold, R.J.M.; Tsui

Proc. Natl. Acad. Sci. U.S.A. 81, 7762-7766, 1984

A/Title: gamma-crystallin family of the mouse lens: structural and evolutionary relations

A/Reference number: A94021; PMID:8508487; PMID:6096855

A/Accession: A02935

A/Molecule type: mRNA

A/Residues: 1-174 <BRES>

A/Cross-references: UNIPROT:P04345

A/Note: the authors translated the codon ATC for residue 36 as Val

Nucleic Acids Res. 12, 4517-4529, 1984

A/Title: Analysis of the mouse gamma-crystallin gene family: assignment of multiple cDNA

A/Reference number: I48353; PMID:84247318; PMID:6330674

A/Accession: I49613

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-174 <RES>

A/Cross-references: GB:K02587; NID:9192771; PIDN:AAA37473.1; PID:9387135

C/Comment: There are at least seven different gamma crystallins identified in mouse lens

C/Genetics:

A/Introns: 3/3; 84/3

C/Superfamily: beta-crystallin

C/Keywords: duplication; eye lens

F/2-40/Domain: crystallin repeat <GK1>

F/41-83/Domain: crystallin repeat <GK2>

F/88-128/Domain: crystallin repeat <GK3>

F/129-168/Domain: crystallin repeat <GK4>

Query Match 69.1%; Score 765.5; DB 1; Length 174;

Best local similarity 77.1%; Pred. No. 5, 1e-65;

Matches 135; Conservative 19; Mismatches 20; Indels 1; Gaps 1;

Qy	1	MGRIFKEDRGFGHGYSCNSDCPPLQYFSCNSIRYLSCGCMWLYERPNYQGHQYFLRR	60
Db	1	MGKITFYEDRGFGHGYSCNSDCPPLQYFSCNSIRYDSCGCMWLYERPNYQGHQYFLRR	60
Qy	61	GDYPDYQGMGFNDISIRSCRLIPQHTGTFNRRIYERDDFRGQWSEITDDCPSLQDRFHLT	120
Db	61	GDYPDYQGMGFNDISIRSCRLIPQHTGTFNRRIYERDDFRGQWSEITDDCPSLQDRFHLT	119
Qy	121	EVHSLNVLKESWVLYEMPSYRGRQYLLRPGYRRLYLDWGMANAKVGSLLRVMDFY	175
Db	120	EYSHAVLEGGCVLIEMPNYRGRQYLLRPGDYYRHHDMGAMDAKVGSLRRVMDLY	174

Search completed: January 14, 2005, 12:07:11
 Job time : 17 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2005, 12:03:35 ; Search time 194 Seconds

(without alignments)
584.272 Million cell updates/sec

Title: US-10-030-605A-21

Perfect score: 1108

Sequence: 1 MGRKFKEDKGFQGHYYSCN.....PNSSVDKLAALHHHHH 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : UniProt 02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	938	84.7	174	1 CRGB_BOVIN	P02526 bos taurus
2	876	79.1	174	1 CRGB_RAT	P10066 rattus norv
3	859	77.3	174	1 CRGB_MOUSE	P03344 mus musculu
4	856	77.3	175	2 O6PHP7	O6php7 mus musculu
5	825	77.3	175	2 AAH56455	AAH56455 mus musculu
6	825	74.5	174	1 CRGB_HUMAN	P07316 homo sapien
7	801	72.3	174	1 CRGA_BOVIN	P02527 bos taurus
8	778.5	70.3	173	1 CRGD_BOVIN	P08209 bos taurus
9	778.5	70.3	173	1 CRGD_RAT	P10067 rattus norv
10	776.5	70.1	174	2 O6PGIO	O6pgio mus musculu
11	776.5	70.1	174	2 AAH57013	AAH57013 mus musculu
12	773.5	69.8	173	1 CRGE_RAT	P02528 rattus norv
13	772.5	69.7	173	1 CRGF_BOVIN	P23005 bos taurus
14	771.5	69.6	173	1 CRGC_RAT	P02529 rattus norv
15	769.5	69.4	173	1 CRGA_RAT	P10065 rattus norv
16	765.5	69.1	173	1 CRGD_MOUSE	P03342 mus musculu
17	762.5	68.8	173	1 CRGE_MOUSE	O03740 mus musculu
18	760.5	68.6	173	1 CRGA_MOUSE	P03345 mus musculu
19	757.5	68.4	173	1 CRGF_RAT	P10068 rattus norv
20	757.5	68.4	174	2 AAH56453	AAH56453 mus musculu
21	752.5	67.9	173	1 CRGF_MOUSE	O9cav3 mus musculu
22	751.5	67.8	173	1 CRGE_BOVIN	O28088 bos taurus
23	747.5	67.5	173	1 CRGC_MOUSE	O61597 mus musculu
24	742.5	65.2	173	1 CRGD_HUMAN	P07320 homo sapien
25	721.5	65.1	173	1 CRGC_HUMAN	P07315 homo sapien
26	710.5	64.1	173	1 CRGA_HUMAN	P18844 homo sapien
27	681	61.5	173	1 CRG2_CHICO	P46645 chilloscylli
28	671	60.6	175	2 O6DKC9	O6dkc9 xenopus lae
29	654	59.0	175	2 O7S2A6	O7s2a6 xenopus lae
30	651	58.8	172	1 CRBS_CHICO	P46646 chilloscylli
31	649	58.6	175	2 O6DJC9	O6djc9 xenopus lae

32	647	58.4	175	2 O6DER7	O6der7 xenopus tro
33	645	58.2	175	1 CRG3_XENLA	P55940 xenopus lae
34	644	58.1	174	2 O9P5T5	O9p5t5 xenopus lae
35	641	57.9	175	2 O8QFV3	O8qfv3 cynops pyrr
36	639	57.7	169	1 CRG2_RANTE	P02531 rana tempor
37	635	57.3	177	2 O93615	O93615 xenopus lae
38	631	56.9	175	1 CRG2_XENLA	O91724 xenopus lae
39	627	56.6	177	1 CRG1_RANCA	O91320 rana catesb
40	621	56.0	175	1 CRG1_XENLA	O06254 xenopus lae
41	616	55.6	177	1 CRG2_XENLA	O91332 rana catesb
42	610	55.1	172	1 CRG4_XENLA	P55941 xenopus lae
43	605	54.6	172	1 CRBT_CHICO	P46647 chilloscylli
44	561	50.6	133	1 CRG1_RANTE	P02530 rana tempor
45	549.5	49.6	173	1 CRBS_CYPCA	P10112 cyprianus ca

ALIGNMENTS

RESULT 1

ID	CRGB_BOVIN	STANDARD;	PRT;	174 AA.
AC	P02526;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-AUG-1988 (Rel. 08, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DB	Gamma crystalalin B (Gamma crystalalin II).			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovine; Bos.			
OX	NCBI_Taxid=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87270760; PubMed=3606621;			
RA	Hay R.B., Woods W.D., Church R.L., Petrash J.M.;			
RT	"cDNA clones encoding bovine gamma-crystallins.";			
RL	Biochem. Biophys. Res. Commun. 146:332-338(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lens;			
RX	MEDLINE=85026663; PubMed=6092016;			
RA	Bhat S.P., Spector A.;			
RT	"Complete nucleotide sequence of a cDNA derived from calf lens gamma-crystallin mRNA: presence of Alu I-like DNA sequences.";			
RL	DNA 3:287-295(1984).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS), AND REVISIONS.			
RX	MEDLINE=81123111; PubMed=7464942;			
RA	Blundell T.L., Lindley P., Miller L., Moss D., Slingsby C., Tickle I.,			
RT	"The molecular structure and stability of the eye lens: X-ray analysis of gamma-crystallin II.";			
RL	Nature 289:771-777(1981).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).			
RX	MEDLINE=84036195; PubMed=6631960;			
RA	Wistow G., Turnell B., Summers L., Slingsby C., Moss D., Miller L.,			
RT	Lindley P., Blundell T.L.;			
RL	"X-ray analysis of the eye lens protein gamma-II crystallin at 1.9-A resolution.";			
RL	J. Mol. Biol. 170:175-202(1983).			
RN	[5]			
RP	X-RAY CRYSTALLOGRAPHY (1.47 ANGSTROMS).			
RA	Najmudin S., Naini V., Dreissen H.P.C., Slingsby C., Blundell T.L.,			
RT	Moss D.S., Lindley P.F.;			
RL	"Structure of the bovine eye lens protein gammaB (gammaII)-crystallin at 1.47 A.";			
RL	Acta Crystallogr. D 49:223-233(1993).			
RN	[6]			
RP	X-RAY CRYSTALLOGRAPHY (1.2 ANGSTROMS).			
RA	Kumaraswamy V.S., Lindley P.F., Slingsby C., Glover I.D.;			
RT	"An eye lens protein-water structure: 1.2-A resolution structure of			

RT gammab-crystallin at 150 K.";
 RL Acta Crystallogr. D 52:611-622 (1996).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=98200466; PubMed=9541393;
 RA Palme S., Jaenicke R., Slingby C.;
 RT "X-ray structures of three interface mutants of gammab-crystallin from
 RT bovine eye lens.";
 RL Protein Sci. 7:611-618 (1998).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT ALA-56.
 RX MEDLINE=98308013; PubMed=9642083;
 RA Palme S., Jaenicke R., Slingby C.;
 RT "Unusual domain pairing in a mutant of bovine lens gammab-
 RT crystallin.";
 RL J. Mol. Biol. 279:1053-1059 (1998).
 CC -1- FUNCTION: Crystallins are the dominant structural components of
 CC the vertebrate eye lens.
 CC -1- DOMAIN: Has a two-domain beta-structure, folded into four very
 CC similar Greek key motifs.
 CC -1- SIMILARITY: Contains 4 beta/gamma crystallin 'Greek key' domains.
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 DR EMBL; X01036; CAA25518.1; -.
 DR EMBL; M16894; AAA30476.1; -.
 DR PIR; A29655; CYBOG.
 DR PDB; 1AMM; X-ray; @=-1-174.
 DR PDB; 1BSL; X-ray; @=-87-174.
 DR PDB; 1GAM; X-ray; A/B=87-172.
 DR PDB; 1GCS; X-ray; @=-1-174.
 DR PDB; 1151; X-ray; A=-1-174.
 DR PDB; 4GCR; X-ray; @=-1-174.
 DR InterPro; IPR01064; Crystallin.
 DR InterPro; IPR011024; G-crystallin_SF.
 DR Pfam; PF00030; Crystallin_2.
 DR PRINTS; PR01357; BGCYSTALLIN.
 DR SMART; SM00247; XTALB; 2.
 DR PROSITE; PS50915; CRYSTALLIN_BETAGAMMA; 4.
 DR 3D-structure; Eye lens protein; Multigene family; Repeat.
 FT INIT MET 0
 FT DOMAIN 1 39 Beta/gamma crystallin 'Greek key' 1.
 FT 40 82 Beta/gamma crystallin 'Greek key' 2.
 FT DOMAIN 83 87 Connecting peptide.
 FT 88 128 Beta/gamma crystallin 'Greek key' 3.
 FT DOMAIN 129 171 Beta/gamma crystallin 'Greek key' 4.
 FT 171 119 T -> S (in Ref. 2).
 FT CONFLICT 119 119
 FT STRAND 2 8
 FT HELIX 9 11
 FT STRAND 12 16
 FT STRAND 22 22
 FT TURN 26 28
 FT STRAND 34 39
 FT STRAND 42 47
 FT TURN 48 50
 FT STRAND 51 57
 FT STRAND 60 62
 FT HELIX 65 68
 FT TURN 69 69
 FT STRAND 77 80
 FT STRAND 89 95
 FT TURN 96 98
 FT STRAND 99 105
 FT STRAND 109 109
 FT HELIX 112 116
 FT STRAND 120 120

FT STRAND 123 128
 FT STRAND 131 136
 FT TURN 137 139
 FT STRAND 140 146
 FT STRAND 149 151
 FT HELIX 154 157
 FT TURN 158 158
 FT STRAND 163 163
 FT STRAND 166 169
 SQ SEQUENCE 174 AA; 20965 MW; 8E404878CA2150A3 CRC64;
 Query Match 84.7%; Score 938; DB 1; Length 174;
 Best Local Similarity 96.0%; Pred. No. 9,1e-79;
 Matches 167; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 2 GRIKFKEDRGFOGHYVSCNSDCENTLQPFYFRCNSIRVLSGCMWLYERPNOGHQYFLRRG 61
 D 1 GKIFVEDRGFOGHYVSCNSDCENTLQPFYFRCNSIRVLSGCMWLYERPNOGHQYFLRRG 60
 QY 62 DYPPYQGMGFNDISIRSCRLIPQHTGTFRRRIYERDDFRQMSBITDDCPSLDRPHLTE 121
 D 61 DYPPYQGMGFNDISIRSCRLIPQHTGTFRRRIYERDDFRQMSBITDDCPSLDRPHLTE 120
 QY 122 VHSINLVESGSMVLYEMPSYRGROYLLRPGERYRLDMGANNAKVGSLRRVMDPY 175
 D 121 VHSINLVESGSMVLYEMPSYRGROYLLRPGERYRLDMGANNAKVGSLRRVMDPY 174
 RESULT 2
 CRGB RAT STANDARD; PRT; 174 AA.
 ID CRGB RAT
 AC P10066;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Gamma crystallin B (Gamma crystallin 1-2).
 GN Name=Crygb;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90236314; PubMed=1970548;
 RA den Dunnen J.T., van Neck J.W., Cremers F.P.M., Lubsen N.H.,
 RA Schoenmakers J.G.G.;
 RT "Isolation and characterization of the rat glutamine synthetase-
 RT encoding gene.";
 RL Gene 87:225-232 (1990).
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87060933; PubMed=3783678;
 RA den Dunnen J.T., Moormann R.J.M., Lubsen N.H., Schoenmakers J.G.G.;
 RT "Concerted and divergent evolution within the rat gamma-crystallin
 RT gene family.";
 RL J. Mol. Biol. 189:37-46 (1986).
 CC -1- FUNCTION: Crystallins are the dominant structural components of
 CC the vertebrate eye lens.
 CC -1- DOMAIN: Has a two-domain beta-structure, folded into four very
 CC similar Greek key motifs.
 CC -1- MISCELLANEOUS: There are six different gamma crystallins
 CC identified in rat lens.
 CC -1- SIMILARITY: Belongs to the beta/gamma crystallin family.
 CC -1- SIMILARITY: Contains 4 beta/gamma crystallin 'Greek key' domains.
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DR EMBL; M19359; AAA40982.1; -.
DR PIR; B24060; B24060.
DR HSSP; P02526; 1MM.
DR RGD; 2420; CrygD.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR011024; G crystallin_SF.
DR Pfam; PF00030; Crystallin_2.
DR PRINTS; PR01367; BGCRCYSTALLIN.
DR SMART; SM00247; XTALbgl; 2.
DR PROSITE; PS50915; CRYSTALLIN BETAGAMMA; 4.
DR Eye lens protein; Multigene family; Repeat.
FT INT MET 0 0
FT DOMAIN 1 39 Beta/gamma crystallin 'Greek key' 1.
FT DOMAIN 40 82 Beta/gamma crystallin 'Greek key' 2.
FT DOMAIN 83 87 Connecting peptide.
FT DOMAIN 88 128 Beta/gamma crystallin 'Greek key' 3.
FT DOMAIN 129 171 Beta/gamma crystallin 'Greek key' 4.
FT CONFLICT 15 15 C -> S (in Ref. 2).
SQ SEQUENCE 174 AA; 20957 MW; 076955A5A94C70C CRC64;

Query Match 79.1%; Score 876; DB 1; Length 174;
Best Local Similarity 88.5%; Pred. No. 5e-73;
Matches 154; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 2 GRIKFKEDRGFGHGYSCNSDCPNLQPYFSRCHSIRVLVSGCMLYERPNYQHGYFLRG 61
DB 1 GKITFFEDRGFGHGYSCNSDCPNLQPYFSRCHSIRVLVSGCMLYERPNYQHGYFLRG 60

QY 62 DYPDYQGMGFNDISIRSCRLIPQHTGTFRRMRYERDDFRGQMSFITDDCSLQDRFHLTE 121
DB 61 DYPDYQGMGFNDISIRSCRLIPQHTGTFRRMRYERDDFRGQMSFITDDCSLQDRFHLTE 120

QY 122 VHSILNVEGSMVLYEMPSYRGROYLRRGEYRRYLDGMANAKVGSRRVWDFY 175
DB 121 IHSILNVEGSMVLYEMPSYRGROYLRRGEYRRYLDGMANAKVGSRRVWDFY 174

RESULT 3
CRGB MOUSE STANDARD; PRT; 174 AA.
AC P04344; O61593;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Gamma crystallin B (Gamma crystallin 3).
GN Name=Crygb;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=102 X C3H; TISSUE=Liver;
RX MEDLINE=94123992; PubMed=829398;
RA Graw J., Liebschtein A., Pieterowski D., Schmitt-John T., Werner T.;
RT "Genomic sequences of murine gamma B- and gamma C-crystallin-encoding
RT genes: promoter analysis and complete evolutionary pattern of mouse,
RT rat and human gamma-crystallins.";
RL Gene 136:145-156(1993).
RN [2]
RP SEQUENCE OF 37-174 FROM N.A.
RX MEDLINE=8508487; PubMed=6096855;
RA Breitman M.L., Lok S., Wistow G., Platigorsky J., Treton J.A.,
RT "Gamma-crystallin family of the mouse lens: structural and
RT evolutionary relationships.";
RL Proc Natl Acad Sci U.S.A. 81:7762-7766(1984).
CC -1- FUNCTION: Crystallins are the dominant structural components of
CC the vertebrate eye lens.
CC -1- DOMAIN: Has a two-domain beta-structure, folded into four very
CC similar Greek key motifs.
CC -1- MISCELLANEOUS: There are six different gamma crystallins
CC identified in mouse lens.

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CC -1- SIMILARITY: Belongs to the beta/gamma-crystallin family.
CC -1- SIMILARITY: Contains 4 beta/gamma crystallin 'Greek key' domains.
CC -1- SIMILARITY: Contains 4 beta/gamma crystallin 'Greek key' domains.
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CC -----
DR EMBL; K02585; AAA37474.1; -.
DR PIR; Z22573; CAA80296.1; -.
DR HSSP; P02526; 1MM.
DR MGD; MGI:88522; Crygb.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR011024; G crystallin_SF.
DR Pfam; PF00030; Crystallin_2.
DR PRINTS; PR01367; BGCRCYSTALLIN.
DR SMART; SM00247; XTALbgl; 2.
DR PROSITE; PS50915; CRYSTALLIN BETAGAMMA; 4.
DR Eye lens protein; Multigene family; Repeat.
FT INT MET 0 0
FT DOMAIN 1 39 Beta/gamma crystallin 'Greek key' 1.
FT DOMAIN 40 82 Beta/gamma crystallin 'Greek key' 2.
FT DOMAIN 83 87 Connecting peptide.
FT DOMAIN 88 128 Beta/gamma crystallin 'Greek key' 3.
FT DOMAIN 129 171 Beta/gamma crystallin 'Greek key' 4.
SQ SEQUENCE 174 AA; 21007 MW; 9D206049E8F327D CRC64;

Query Match 77.5%; Score 859; DB 1; Length 174;
Best Local Similarity 86.2%; Pred. No. 1.9e-71;
Matches 150; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 2 GRIKFKEDRGFGHGYSCNSDCPNLQPYFSRCHSIRVLVSGCMLYERPNYQHGYFLRG 61
DB 1 GKITFFEDRGFGHGYSCNSDCPNLQPYFSRCHSIRVLVSGCMLYERPNYQHGYFLRG 60

QY 62 DYPDYQGMGFNDISIRSCRLIPQHTGTFRRMRYERDDFRGQMSFITDDCSLQDRFHLTE 121
DB 61 DYPDYQGMGFNDISIRSCRLIPQHTGTFRRMRYERDDFRGQMSFITDDCSLQDRFHLTE 120

QY 122 VHSILNVEGSMVLYEMPSYRGROYLRRGEYRRYLDGMANAKVGSRRVWDFY 175
DB 121 IHSILNVEGSMVLYEMPSYRGROYLRRGEYRRYLDGMANAKVGSRRVWDFY 174

RESULT 4
Q6PHP7 PRELIMINARY; PRT; 175 AA.
ID Q6PHP7;
AC Q6PHP7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Crystallin, gamma B.
GN Name=Crygb;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.T., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguoliano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Crystallins are the dominant structural components of
 CC the vertebrate eye lens (By similarity).
 CC -1- DOMAIN: Has a two-domain beta-structure, folded into four very
 CC similar Greek key motifs (By similarity).
 CC -1- SIMILARITY: Belongs to the beta/gamma-crystallin family.
 DR EMBL: BC056455; AAH56455.1; -;
 DR InterPro: IPR01064; Crystallin.
 DR InterPro: IPR01024; G_crystallin_SF.
 DR Pfam: PF00030; Crystall1; 2.
 DR PRINTS: PR01367; BGCRCRYSTALLIN.
 DR SMART: SM00247; XTALBP; 2.
 DR PROSITE: PS50915; CRYSTALLIN_BETAGAMMA; 4.
 SQ SEQUENCE 175 AA; 21086 MW; 1E39B15A0AAB175D CRC64;
 Query Match 77.3%; Score 856; DB 2; Length 175;
 Best Local Similarity 85.7%; Pred. No. 3.6e-71;
 Matches 150; Conservative 11; Mismatches 14; Indels 0; Gaps 0;
 QY 1 MGRKFKEDRGFGQHYSCNSDCPNLQPYFSCNSIRVLSGCMWLYERPNOGHQYFLRR 60
 DB 1 MGRKTFEDRSFGRCYECSSDCPNLQPYFSCNSIRVLSGCMWLYERPNOGHQYFLRR 60
 QY 121 EVHSLNVLEGSWVLYEMPSTRGRQYLLRPGEYRRLDGMANAKVGSFRVMDYF 175
 DB 121 EIHSLNVMEGCVLYEMPSTRGRQYLLRPGEYRRLDGMANAKVGSFRVMDYF 175
 RESULT 5
 AAH56455 PRELIMINARY; PRT; 175 AA.
 AC AAH56455;
 DT 10-MAY-2004 (TRENBLrel. 27, Created)
 DT 10-MAY-2004 (TRENBLrel. 27, Last sequence update)
 DT 10-MAY-2004 (TRENBLrel. 27, Last annotation update)
 DE Crystallin, gamma B.
 GN CRYGB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Heile F.,
 RA Dichtchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshitsuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC056455; AAH56455.1; -;
 SQ SEQUENCE 175 AA; 21086 MW; 1E39B15A0AAB175D CRC64;
 Query Match 77.3%; Score 856; DB 2; Length 175;
 Best Local Similarity 85.7%; Pred. No. 3.6e-71;
 Matches 150; Conservative 11; Mismatches 14; Indels 0; Gaps 0;
 QY 1 MGRKFKEDRGFGQHYSCNSDCPNLQPYFSCNSIRVLSGCMWLYERPNOGHQYFLRR 60
 DB 1 MGRKTFEDRSFGRCYECSSDCPNLQPYFSCNSIRVLSGCMWLYERPNOGHQYFLRR 60
 QY 121 EVHSLNVLEGSWVLYEMPSTRGRQYLLRPGEYRRLDGMANAKVGSFRVMDYF 175
 DB 121 EIHSLNVMEGCVLYEMPSTRGRQYLLRPGEYRRLDGMANAKVGSFRVMDYF 175
 RESULT 6
 CRGB_HUMAN STANDARD; PRT; 174 AA.
 ID CRGB_HUMAN
 AC P07316;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Gamma crystallin B (Gamma crystallin 1-2).
 GN Name-CRYGB; Synonyms-CRYG2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=86056977; PubMed=4065573;
 RA den Dunnen J.T., Wootman R.J.M., Cremers F.P.M., Schoenmakers J.G.G.,
 RT "Two human gamma-crystallin genes are linked and riddled with Alu-
 RT repeats.";
 RL Gene 38:197-204 (1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=89378747; PubMed=2777080;
 RA den Dunnen J.T., van Neck J.W., Cremers F.P., Lubsen N.H.,
 RA Schoenmakers J.G.G.,
 RT "Nucleotide sequence of the rat gamma-crystallin gene region and
 RT comparison with an orthologous human region.";
 RL Gene 78:201-213 (1989).
 RN [3]
 RP 3D-STRUCTURE MODELING.
 RC MEDLINE=22395646; PubMed=12507494; DOI=10.1016/S0006-291X(02)02895-4;
 RA Salim A., Zaidi Z.H.,
 RT "Homology models of human gamma-crystallins: structural study of the
 RT extensive charge network in gamma-crystallins.";
 RL Biochem. Biophys. Res. Commun. 300:624-630(2003).
 CC -1- FUNCTION: Crystallins are the dominant structural components of

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CC      the vertebrate eye lens.
CC      -1- SUBUNIT: Monomer (by similarity).
CC      -1- DOMAIN: Has a two-domain beta-structure, folded into four very
CC      similar Greek key motifs.
CC      -1- SIMILARITY: Belongs to the beta/gamma-crystallin family.
CC      -1- SIMILARITY: Contains 4 beta/gamma-crystallin 'Greek key' domains.
CC      -----
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CC      entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC      or send an email to license@ebi.ac.uk).
CC      -----
CC      EMBL: M11971; AAAS2113.1; -.
CC      EMBL: M11970; AAAS2113.1; JOINED.
CC      EMBL: M19364; AAAS2109.1; -.
CC      PIR: A24520; CYHUG1.
CC      PDB: 1LEU; Model: A-1-174.
CC      Genew: HGNC:2409; CRYGB.
CC      MIM: 123670; -.
CC      GO: GO:0005212; F:structural constituent of eye lens; NAS.
CC      InterPro: IPR01064; Crystallin.
CC      InterPro: IPR011024; G-crystallin_SF.
CC      Pfam: PF00030; Crystallin_2.
CC      PRINTS: PR01367; BGCRCYSTALIN.
CC      SMART: SM00247; XTALbg; 2.
CC      PROSITE: PS50915; CRYSTALLIN BETAGAMMA; 4.
CC      3D-structure: Eye lens protein, Multigene family; Repeat.
CC      INIT MET 0
CC      DOMAIN 1 39 Beta/gamma crystallin 'Greek key' 1.
CC      FT 40 82 Beta/gamma crystallin 'Greek key' 2.
CC      FT 83 87 Connecting peptide.
CC      FT 88 128 Beta/gamma crystallin 'Greek key' 3.
CC      FT 129 171 Beta/gamma crystallin 'Greek key' 4.
CC      DOMAIN 129 171
CC      SEQUENCE 174 AA; 20776 MW; 6533BE9001EBBFCC CRC64;

Query Match 74.5%; Score 825; DB 1; Length 174;
Best Local Similarity 81.6%; Pred. No. 2.6e-68;
Matches 142; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 2 GRIKFKEDRGFGHGYHCNSDCPNLQPYFSRCNSIRVLSGCMWLYERNYQHOYFLRRG 61
DB 1 GKIFTEBRARQGRSYECTTCPNLQPYFSRCNSIRVLSGCMWLYERNYQHOYFLRRG 60
QY 62 DYPDYQGMGPNDSIRSCRLIPQHTGTFRMRIYERDPRGQMSITDDCPSLQDRFHLTE 121
DB 61 EYDPDYQGMGPNDSIRSCRLIPHSQAYRMKIYDRDELRGQMSITDDCPSLQDRFHLTE 120
QY 122 VHSILNVLGSGVLYEMPSYRGROYLIRPGEYRRYLDGMANAKVGLRRVMDFY 175
DB 121 IHSILNVLGSGVLYEMPSYRGROYLIRPGEYRRYLDGMANAKVGLRRVMDFY 174

RESULT 7
CRGA BOVIN STANDARD; PRT; 174 AA.
ID CRGA_BOVIN
AC P02527;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Gamma crystallin A (Gamma crystallin IIV).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxId=9913;
RN (1)
RP SEQUENCE.
RX MEDLINE=73054483; PubMed=4674126;
RA Croft L.R.;
RT "The amino acid sequence of gamma-crystallin (fraction II) from calf

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RT lens.";
RL Biochem. J. 128:961-970 (1972).
CC -1- FUNCTION: Crystallins are the dominant structural components of
CC the vertebrate eye lens.
CC -1- DOMAIN: Has a two-domain beta-structure, folded into four very
CC similar Greek key motifs.
CC -1- SIMILARITY: Belongs to the beta/gamma-crystallin family.
CC -1- SIMILARITY: Contains 4 beta/gamma-crystallin 'Greek key' domains.
CC HSP; P02526; IISL.
DR InterPro: IPR01064; Crystallin.
DR InterPro: IPR011024; G-crystallin_SF.
DR Pfam: PF00030; Crystallin_2.
DR PRINTS: PR01367; BGCRCYSTALIN.
DR SMART: SM00247; XTALbg; 2.
DR PROSITE: PS50915; CRYSTALLIN BETAGAMMA; 4.
KW Direct protein sequencing; Eye lens protein; Multigene family; Repeat.
FT DOMAIN 1 39 Beta/gamma crystallin 'Greek key' 1.
FT 40 82 Beta/gamma crystallin 'Greek key' 2.
FT 83 87 Connecting peptide.
FT 88 128 Beta/gamma crystallin 'Greek key' 3.
FT DOMAIN 129 171 Beta/gamma crystallin 'Greek key' 4.
FT SEQUENCE 174 AA; 21003 MW; B39093A105E2CEBF CRC64;

Query Match 72.3%; Score 801; DB 1; Length 174;
Best Local Similarity 82.8%; Pred. No. 4.3e-66;
Matches 144; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 2 GRIKFKEDRGFGHGYHCNSDCPNLQPYFSRCNSIRVLSGCMWLYERNYQHOYFLRRG 61
DB 1 GKIFTEBRARQGRSYECTTCPNLQPYFSRCNSIRVLSGCMWLYERNYQHOYFLRRG 60
QY 62 DYPDYQGMGPNDSIRSCRLIPQHTGTFRMRIYERDPRGQMSITDDCPSLQDRFHLTE 121
DB 61 NYDPDYQGMGPNDSIRSCRLIPQHTGTFRMRIYERDPRGQMSITDDCPSLQDRFHLTE 120
QY 122 VHSILNVLGSGVLYEMPSYRGROYLIRPGEYRRYLDGMANAKVGLRRVMDFY 175
DB 121 VHSILNVLGSGVLYEMPSYRGROYLIRPGEYRRYLDGMANAKVGLRRVMDFY 174

RESULT 8
CRGD BOVIN STANDARD; PRT; 173 AA.
ID CRGD_BOVIN
AC P08209; Q28089;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Gamma crystallin D (Gamma crystallin IIB).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxId=9913;
RN (1)
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Lens;
RX MEDLINE=95010404; PubMed=7925695;
RA Hay R.E., Andley U.P., Petrasch J.M.;
RT "Expression of recombinant bovine gamma B-, gamma C- and gamma D-
RT crystallins and correlation with native proteins.";
RL Exp. Eye Res. 58:573-584 (1994).
RN (2)
RP SEQUENCE OF 1-156 FROM N.A.
RC TISSUE=Lens;
RX MEDLINE=87270760; PubMed=3606621;
RA Hay R.E., Woods W.D., Church R.L., Petrasch J.M.;
RT "cDNA clones encoding bovine gamma-crystallins.";
RL Biochem. Biophys. Res. Commun. 146:332-338 (1987).
RN (3)
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
RX Chirgadze Y.N., Driessen H.P.C., Wright G., Slingsby C., Hay R.E.,
RA Lindley P.F.;
RT "Structure of bovine eye lens gammaD (gammaIIB)-crystallin at 1.95

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RT A.";
 RL Acta Crystallogr. D 52:712-721(1996).
 CC -1- FUNCTION: Crystallins are the dominant structural components of
 CC the vertebrate eye lens.
 CC -1- DOMAIN: Has a two-domain beta-structure, folded into four very
 CC similar Greek key motifs.
 CC -1- SIMILARITY: Belongs to the beta/gamma-crystallin 'Greek key' domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L27070; AAA8995.1; -
 DR EMBL: M16895; AAB59282.1; -
 DR PDB: 1ELP; X-ray; A/B=1-173.
 DR InterPro: IPR001064; Crystallin.
 DR InterPro: IPR011024; G-crystallin_SF.
 DR Pfam: PF00030; Crystall; 2.
 DR PRINTS: PRO1367; BGCRYSTALIN.
 DR SMART: SM00247; XTALBg; 2.
 DR PROSITE: PS50915; CRYSTALIN BETAGAMMA; 4.
 DR 3D-structure; Direct protein sequencing; Eye lens protein;
 DR Multigene family; Repeat.
 DR INIT MET 0
 FT DOMAIN 1 39 Beta/gamma crystallin 'Greek key' 1.
 FT DOMAIN 40 82 Beta/gamma crystallin 'Greek key' 2.
 FT DOMAIN 83 86 Connecting peptide.
 FT DOMAIN 87 127 Beta/gamma crystallin 'Greek key' 3.
 FT DOMAIN 128 170 Beta/gamma crystallin 'Greek key' 4.
 FT CONFLICT 75 75 V -> I (in Ref. 2).
 FT STRAND 2 8
 FT HELIX 9 11
 FT STRAND 12 18
 FT STRAND 22 22
 FT TURN 26 28
 FT STRAND 34 39
 FT STRAND 42 45
 FT TURN 49 50
 FT STRAND 54 57
 FT STRAND 60 62
 FT HELIX 65 68
 FT TURN 69 69
 FT STRAND 77 80
 FT STRAND 88 94
 FT TURN 95 97
 FT STRAND 98 104
 FT STRAND 108 108
 FT HELIX 111 114
 FT TURN 115 115
 FT STRAND 119 119
 FT STRAND 122 127
 FT STRAND 130 135
 FT TURN 136 138
 FT STRAND 148 145
 FT STRAND 149 150
 FT HELIX 153 156
 FT TURN 157 157
 FT STRAND 162 162
 FT STRAND 165 168
 FT SEQUENCE 173 AA; 20735 MW; D9D853EB3B3F7B5F CRC64;
 Query Match 70.3%; Score 778.5; DB 1; Length 173;
 Best Local Similarity 78.2%; Pred. No. 5.2e-64;
 Matches 136; Conservative 17; Mismatches 20; Indels 1; Gaps 1;
 QY 2 GRIKFKEDRGFGHYHSGNSDCPNLQPYFSRCNSIRVLSCGWMLYERPNTQGHQYFLARG 61
 Db 1 GKIFVEYDRGFGHNYECSSDHSNLTQPYLGRCNSVRVDSCGMWITYEGPNTLGQYFLARG 60

QY 62 DYPYQMGWFNDISRCRLIPQHTGFRMKIYERDDFRQMSBITDDCSLQDRFLRTE 121
 Db 61 DYPYQMGWGLNDISVRCRLIP-HAGSHRLRLYEREDYRQGMIEITBDCSSLQDRFPFNE 119
 QY 122 VHSINLVGSGVWLVEMPSYRGROYLNRPGYRRYLDWGMANNAVXGSLRRVNDPF 175
 Db 120 IHSINLVGSGVWLVLEPNYRGROYLNRPGYRRYLDWGMANNAVXGSLRRVNDY 173
 RESULT 9
 ID CRGD RAT STANDARD; PRT; 173 AA.
 AC P10067;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Gamma crystallin D (Gamma crystallin 2-2).
 GN Name=Crygd;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90236314; PubMed=1970548;
 RA den Dunnen J.T., van Neck J.W., Cremers F.P.M., Lubben N.H.,
 RA Schoenmakers J.G.G.;
 RT "Isolation and characterization of the rat glutamine synthetase-
 RT encoding gene";
 RT Gene 87:225-232(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87060933; PubMed=3783678;
 RA den Dunnen J.T., Moorman R.J.M., Lubben N.H., Schoenmakers J.G.G.;
 RT "Concerted and divergent evolution within the rat gamma-crystallin
 RT gene family";
 RT J. Mol. Biol. 189:37-46(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Sprague-Dawley; TISSUE=lens;
 RX MEDLINE=95151850; PubMed=7849105;
 RA Ooki K., Amuro N., Shimizu Y., Okazaki T.;
 RT "High level expression of rat gamma-D-crystallin in Escherichia
 RT coli";
 RT Biochimie 76:398-403(1994).
 CC -1- FUNCTION: Crystallins are the dominant structural components of
 CC the vertebrate eye lens.
 CC -1- DOMAIN: Has a two-domain beta-structure, folded into four very
 CC similar Greek key motifs.
 CC -1- MISCELLANEOUS: There are six different gamma crystallins
 CC identified in rat lens.
 CC -1- SIMILARITY: Belongs to the beta/gamma-crystallin 'Greek key' domains.
 CC -1- SIMILARITY: Contains 4 beta/gamma crystallin 'Greek key' domains.
 CC -----
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 CC -----
 DR EMBL: M19359; AAA40984.1; -
 DR EMBL: X57169; AAA40458.1; -
 DR PIR: D24060; D24060.
 DR HSSP: P02528; IASD.
 DR RGD: 2422; Crygd.
 DR InterPro: IPR001064; Crystallin.
 DR InterPro: IPR011024; G-crystallin_SF.
 DR Pfam: PF00030; Crystall; 2.
 DR PRINTS: PRO1367; BGCRYSTALIN.
 DR SMART: SM00247; XTALBg; 2.

DR PROSITE: PS50915; CRYSTALLIN BETAGAMMA; 4.
KW Eye lens protein; Multigene Family; Repeat.
FT INIT_MET 0
FT DOMAIN 1 39 Beta/gamma crystallin 'Greek key' 1.
FT DOMAIN 40 82 Beta/gamma crystallin 'Greek key' 2.
FT DOMAIN 83 86 Connecting peptide.
FT DOMAIN 87 127 Beta/gamma crystallin 'Greek key' 3.
FT DOMAIN 128 170 Beta/gamma crystallin 'Greek key' 4.
SQ SEQUENCE 173 AA; 20972 MW; 93082D42D80F4117 CRC64;

Query Match 70.3%; Score 778.5; DB 1; Length 173;
Best Local Similarity 78.2%; Pred. No. 5,2e-64;
Matches 136; Conservative 19; Mismatches 18; Indels 1; Gaps 1;

QY 2 GRIKKEKRGFGQHYHSCNSDCPNLOPYFRSCNSIRVLSCGMLYERNYQGHQYFLRR 61
DB 1 MGKTFYEDRGFGGRHYECSTDSHNLQPYFRSCNSVRVDSGCMMLYEQNPFGCCQYFLRR 60
QY 62 DYDPDYQOMMGFNSDSVRSCLRLPQHTGTFMRIRYERDDFRGQMSITDDCPSLQDRFHLT 121
DB 61 DYDPDYQOMMGFNSDSVRSCLRLP-HAGSHRIRLRYEREDYRGQVETTEDCPSLQDRFHLT 119
QY 122 VHSLSLVLEGSWVLYEMPSYRGROYLLRPGERYRRLDGMANNAKYGSLRRVMDY 175
DB 120 EYLSLVLEGSWVLYEMTNYRGROYLLRPGERYRRLDGMANNAKYGSLRRVMDY 173

RESULT 10
Q6PG10 PRELIMINARY; PRT; 174 AA.
AC 06PG10;
DT 05-JUN-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Crystallin, gamma D.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshlyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bogak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RU Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Crystallins are the dominant structural components of
the vertebrate eye lens (By similarity).
CC -1- DOMAIN: Has a two-domain beta-structure, folded into four very
similar Greek key motifs (By similarity).
CC -1- SIMILARITY: Belongs to the beta/gamma-crystallin family.

DR EMBL: BC057013; AAH57013.1; -
DR InterPro: IPR001064; Crystallin.
DR InterPro: IPR011024; Crystallin_SF.
DR Pfam: PF00030; Crystallin; 2.
DR PRINTS: PR01367; BGCYSTALLIN.
DR SMART: SM00247; XTALBG; 2.
DR PROSITE: PS50915; CRYSTALLIN BETAGAMMA; 4.
SQ SEQUENCE 174 AA; 21118 MW; 1AFC29C0269835A1 CRC64;

Query Match 70.1%; Score 776.5; DB 2; Length 174;
Best Local Similarity 77.1%; Pred. No. 8e-64;
Matches 135; Conservative 21; Mismatches 18; Indels 1; Gaps 1;

QY 1 MGRKFKEDRGFGQHYHSCNSDCPNLOPYFRSCNSIRVLSCGMLYERNYQGHQYFLRR 60
DB 1 MGKTFYEDRGFGGRHYECSTDSHNLQPYFRSCNSVRVDSGCMMLYEQNPFGCCQYFLRR 60
QY 61 GDYDPDYQOMMGFNSDSVRSCLRLPQHTGTFMRIRYERDDFRGQMSITDDCPSLQDRFHLT 120
DB 61 GDYDPDYQOMMGFNSDSVRSCLRLP-HAGSHRIRLRYEREDYRGQVETTEDCPSLQDRFHLT 119
QY 121 EVHSLSLVLEGSWVLYEMPSYRGROYLLRPGERYRRLDGMANNAKYGSLRRVMDY 175
DB 120 EYLSLVLEGSWVLYEMTNYRGROYLLRPGERYRRLDGMANNAKYGSLRRVMDY 174

RESULT 11
AAH57013 PRELIMINARY; PRT; 174 AA.
AC AAH57013;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE Crystallin, gamma D.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shennan C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshlyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bogak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RU Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC057013; AAH57013.1; -
SQ SEQUENCE 174 AA; 21118 MW; 1AFC29C0269835A1 CRC64;

Query Match 70.1%; Score 776.5; DB 2; Length 174;
Best Local Similarity 77.1%; Pred. No. 8e-64;
Matches 135; Conservative 21; Mismatches 18; Indels 1; Gaps 1;

DT 15-JUN-1998 (Rel. 36, last sequence update)
 DT 01-OCT-2004 (Rel. 45, last annotation update)
 DE Gamma crystallin IVA (Gamma crystallin IVA).
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovinae; Bos.
 NCBI_TaxID=9913;
 RN (1)
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=89293855; PubMed=2738925;
 RA White H.E., Driesen H.P.C., Slingsby C., Moss D.S., Lindley P.F.;
 RT "Packing interactions in the eye-lens. Structural analysis, internal
 RT symmetry and lattice interactions of bovine gamma IVA-crystallin."
 RL J. Mol. Biol. 207:217-235 (1989).
 (2)
 RP SEQUENCE FROM N.A. AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=98035705; PubMed=9367641;
 RA Norledge B.V., Hay R.E., Bateman O.A., Slingsby C., Driesen H.P.C.;
 RT "Towards a molecular understanding of phase separation in the lens: a
 RT comparison of the X-ray structures of two high TC gamma-crystallins,
 RT gammaE and gammaF, with two low TC gamma-crystallins, gammaB and
 RT gammaD."
 RL Exp. Eye Res. 65:609-630 (1997).
 CC -1- FUNCTION: Crystallins are the dominant structural components of
 CC the vertebrate eye lens.
 CC -1- DOMAIN: Has a two-domain beta-structure, folded into four very
 CC similar Greek key motifs.
 CC -1- SIMILARITY: Belongs to the beta/gamma-crystallin family.
 CC PDB: 1A45; X-ray; @=1-173.
 DR PDB: 1M8U; X-ray; A=1-173.
 DR InterPro: IPR001064; Crystallin.
 DR InterPro: IPR011024; G_gamma-crystallin_SF.
 DR Pfam: PF00030; Crystallin_2.
 DR PRINTS: PRO1367; BGCRCRYSTALLIN.
 DR SMART: SM00247; XTALB; 2.
 DR PROSITE: PS50915; CRYSTALLIN_BETAGAMMA; 4.
 DR 3D-structure; Eye lens protein; Multigene family; Repeat.
 KW INT MET 0
 FT DOMAIN 1 39 Beta/gamma crystallin 'Greek key' 1.
 FT DOMAIN 83 86 Beta/gamma crystallin 'Greek key' 2.
 FT DOMAIN 87 127 Connecting peptide.
 FT DOMAIN 128 170 Beta/gamma crystallin 'Greek key' 3.
 FT TURN 2 8 Beta/gamma crystallin 'Greek key' 4.
 FT TURN 9 11
 FT STRAND 12 18
 FT STRAND 22 22
 FT TURN 26 28
 FT STRAND 34 39
 FT STRAND 41 45
 FT STRAND 48 50
 FT STRAND 54 57
 FT STRAND 60 62
 FT TURN 65 69
 FT STRAND 77 81
 FT STRAND 88 92
 FT HELIX 95 97
 FT STRAND 101 104
 FT STRAND 108 108
 FT TURN 112 114
 FT STRAND 122 127
 FT STRAND 130 133
 FT STRAND 142 145
 FT STRAND 148 150
 FT STRAND 153 156
 FT HELIX 157 157
 FT TURN 157 157
 FT STRAND 165 168
 SQ SEQUENCE 173 AA; 20955 MW; AC19CA6CC323EC90 CRC64;

Query Match 69.7%; Score 772.5; DB 1; Length 173;
 Best Local Similarity 78.7%; Pred. No. 1.9e-63;

Matches 137; Conservative 16; Mismatches 20; Indels 1; Gaps 1;
 QY 2 GRIFKDRGPOGHYSCNSDCLPLOPYFSCNSIRLSCGMLYKRPYOGHGYFLRG 61
 DB 1 GKIFVEDRGPOGHYSCSDSHSLQYFSCNSIRVDSGCMWLYEOPNQGPOYFLRG 60
 QY 62 DYPDQGMGPNDSIRSCRLIPHOHTGFRMRIRYRDQFQMSBITDCCSLQORFLUTE 121
 DB 61 DYPDQGMGPNDSIRSCRLIPHTGSHRLRIRYREDYRQGMWBITDCCSLHRRFSE 119
 QY 122 VHSINLVGSGWVLYEMPSYRGROYLRLPGEXRYRLDWGAMNAKYSLRVWDFY 175
 DB 120 IHSFNVLGGMWVLYEMTNVGRGYLRLPGDYRHYDGMATNARVGSIRRAVDYF 173
 RESULT 14
 ID CRGC RAT STANDARD; PRT; 173 AA.
 AC P02529;
 DT 21-JUN-1986 (Rel. 01, Created)
 DT 01-AUG-1991 (Rel. 19, last sequence update)
 DT 01-OCT-2004 (Rel. 45, last annotation update)
 DE Gamma crystallin C (Gamma crystallin 2-1).
 GN Name=Crygc;
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90236314; PubMed=1970548;
 RA den Dunnen J.T., van Neck J.W., Cremers F.P.M., Lubsen N.H.;
 RA Schoenmakers J.G.G.;
 RT "Isolation and characterization of the rat glutamine synthetase-
 RT encoding gene."
 RL Gene 87:225-232 (1990).
 (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87060933; PubMed=3783678;
 RA den Dunnen J.T., Moormann R.J.M., Lubsen N.H., Schoenmakers J.G.G.;
 RT "Concerted and divergent evolution within the rat gamma-crystallin
 RT gene family."
 RL J. Mol. Biol. 189:37-46 (1986).
 (3)
 RP SEQUENCE OF 4-173 FROM N.A.
 RX MEDLINE=83091061; PubMed=6294661;
 RA Moormann R.J.M., den Dunnen J.T., Bloemendal H., Schoenmakers J.G.G.;
 RT "Extensive intragenic sequence homology in two distinct rat lens
 RT gamma-crystallin cDNAs suggests duplications of a primordial gene."
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6876-6880 (1982).
 CC -1- FUNCTION: Crystallins are the dominant structural components of
 CC the vertebrate eye lens.
 CC -1- DOMAIN: Has a two-domain beta-structure, folded into four very
 CC similar Greek key motifs.
 CC -1- MISCELLANEOUS: There are six different gamma crystallins
 CC identified in rat lens.
 CC -1- SIMILARITY: Belongs to the beta/gamma-crystallin family.
 CC -1- SIMILARITY: Contains 4 beta/gamma crystallin 'Greek key' domains.
 CC -----
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 CC -----
 DR EMBL: M19359; AAA40983.1; -;
 DR EMBL: J00717; AAA40986.1; -;
 DR PIR: A02934; CYRTG2.
 DR PIR: I83432; I83432.
 DR HSSP: P02526; IAMM.
 DR RGD: 2421; Crygc.

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DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR011024; G-crystallin_SF.
DR Pfam; PF000030; Crystall; 2.
DR PRINTS; PR01367; BGCYSTALLIN.
DR SMART; SM00247; XTALBg; 2.
DR PROSITE; PS50915; CRYSTALLIN_BETAGAMMA; 4.
DR Eye lens protein; Multigene family; Repeat.
KW INIT MET
FT DOMAIN 1 39 Beta/gamma crystallin 'Greek key' 1.
FT DOMAIN 40 82 Beta/gamma crystallin 'Greek key' 2.
FT DOMAIN 83 86 Connecting peptide.
FT DOMAIN 87 127 Beta/gamma crystallin 'Greek key' 3.
FT DOMAIN 128 170 Beta/gamma crystallin 'Greek key' 4.
FT CONFLICT 15 15 C -> S (in Ref. 2 and 3).
FT CONFLICT 35 35 I -> V (in Ref. 2 and 3).
FT CONFLICT 83 83 H -> R (in Ref. 3).
FT CONFLICT 87 87 H -> Q (in Ref. 3).
FT CONFLICT 168 169 RV -> SA (in Ref. 3).
SQ SEQUENCE 173 AA; 20819 MW; 1F7E7324A8BEFDB CRC64;

Query Match
Best Local Similarity 78.2%; Score 771.5; DB 1; Length 173;
Matches 136; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

QY 2 GRIKFKEDRGFGQHYHSCNSDCPNLQPYFRCNSIRVLSGCMWLYERPVGQHYFLRG 61
DB 1 GKITFYEDRGFGRCYECSDCPNLTQYFRCNSIRVDSGCMWLYERPVGQHYFLRG 60
QY 62 DYDPYQOMMGFNSIRSCRLIPQHTGTFPMRIYERDDPFGOMSETDDCPSLDRPHLITE 121
DB 61 DYDPYQOMMGFNSIRSCRLIP-HTGSIRMLYERKEDHNGVMMLSEDCSCIDRPHLSE 119
QY 122 VHSILNVLGSGWVLYEMPSYRGQYLLRPGYRRLYLDGMANAKVGSILRRVMDFY 175
DB 120 VHSILNVLGSGWVLYEMPNYRGQYLLRPGYRRLYHDGMADKAGSLRRVMDLY 173

RESULT 15
RCGA RAT STANDARD; PRT; 173 AA.
ID P10065;
DT 01-MAR-1989 (Rel. 10. Created)
DT 01-AUG-1991 (Rel. 19. Last sequence update)
DT 01-OCT-2004 (Rel. 45. Last annotation update)
DE Gamma crystallin A (Gamma crystallin 1-1).
GN Name=Cryga;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_taxid=10116;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=90236314; PubMed=1970548;
RA den Dunnen J.T., Moormann R.J.M., Lubben N.H., Schoenmakers J.G.G.;
RA Schoenmakers J.G.G.;
RT "Isolation and characterization of the rat glutamine synthetase-
RT encoding gene."
RL Gene 87:225-232 (1990).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=87060933; PubMed=3783578;
RA den Dunnen J.T., Moormann R.J.M., Lubben N.H., Schoenmakers J.G.G.;
RT "Concerted and divergent evolution within the rat gamma-crystallin
RT gene family."
RL J. Mol. Biol. 189:37-46 (1986).
CC -1- FUNCTION: Crystallins are the dominant structural components of
CC the vertebrate eye lens.
CC -1- DOMAIN: Has a two-domain beta-structure, folded into four very
CC similar Greek key motifs.
CC -1- MISCELLANEOUS: There are six different gamma crystallins
CC identified in rat lens.
CC -1- SIMILARITY: Belongs to the beta/gamma-crystallin family.
CC -1- SIMILARITY: Contains 4 beta/gamma crystallin 'Greek key' domains.

```

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CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; M19359; AAA40981.1; -.
CC PIR; A24060; A24060.
CC HSSP; P02526; 1AMM.
CC RGD; 2419; Cryga.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR011024; G-crystallin_SF.
DR Pfam; PF000030; Crystall; 2.
DR PRINTS; PR01367; BGCYSTALLIN.
DR SMART; SM00247; XTALBg; 2.
DR PROSITE; PS50915; CRYSTALLIN_BETAGAMMA; 4.
DR Eye lens protein; Multigene family; Repeat.
KW INIT MET
FT DOMAIN 1 39 Beta/gamma crystallin 'Greek key' 1.
FT DOMAIN 40 82 Beta/gamma crystallin 'Greek key' 2.
FT DOMAIN 83 86 Connecting peptide.
FT DOMAIN 87 127 Beta/gamma crystallin 'Greek key' 3.
FT DOMAIN 128 170 Beta/gamma crystallin 'Greek key' 4.
FT CONFLICT 15 15 C -> S (in Ref. 2).
SQ SEQUENCE 173 AA; 20962 MW; A561FCFA70F8620 CRC64;

Query Match
Best Local Similarity 77.6%; Score 769.5; DB 1; Length 173;
Matches 135; Conservative 20; Mismatches 18; Indels 1; Gaps 1;

QY 2 GRIKFKEDRGFGQHYHSCNSDCPNLQPYFRCNSIRVLSGCMWLYERPVGQHYFLRG 61
DB 1 GKITFYEDRGFGRCYECSDCPNLTQYFRCNSIRVDSGCMWLYERPVGQHYFLRG 60
QY 62 DYDPYQOMMGFNSIRSCRLIPQHTGTFPMRIYERDDPFGOMSETDDCPSLDRPHLITE 121
DB 61 DYDPYQOMMGFNSIRSCRLIP-YTSSIRILYERDYGALVELTEDSCCHDRPHLSE 119
QY 122 VHSILNVLGSGWVLYEMPSYRGQYLLRPGYRRLYLDGMANAKVGSILRRVMDFY 175
DB 120 IYSMVLNVLGSGWVLYEMPNYRGQYLLRPGDYRRLYHDGMADKAGSLRRVMDLY 173

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Search completed: January 14, 2005, 12:10:32
 Job time : 196 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2005, 12:03:35 : Search time 21 Seconds

(without alignments)
622.126 Million cell updates/sec

Title: US-10-030-605A-21

Perfect score: 1108

Sequence: 1 MGRIRKREKRGFGQHYHSCN.....PNSSVDKLAALHHHHHH 197

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	300	27.1	205	2 US-08-729-152-8	Sequence 8, Appl
2	281.5	25.4	215	2 US-08-729-152-1	Sequence 1, Appl
3	100	9.0	42	1 US-08-664-449-39	Sequence 39, Appl
4	86	7.8	378	4 US-08-979-847B-122	Sequence 12, Appl
5	86	7.8	398	4 US-08-979-847B-121	Sequence 11, Appl
6	82	7.4	320	2 US-08-757-653-163	Sequence 163, Appl
7	82	7.4	320	2 US-08-823-516-61	Sequence 61, Appl
8	82	7.4	320	3 US-08-759-038-102	Sequence 102, Appl
9	82	7.4	320	3 US-08-758-314-102	Sequence 102, Appl
10	82	7.4	320	4 US-08-684-938-102	Sequence 102, Appl
11	82	7.4	320	4 US-08-308-825A-102	Sequence 102, Appl
12	82	7.4	320	4 US-09-940-244-61	Sequence 61, Appl
13	80.5	7.3	655	4 US-09-270-767-43477	Sequence 43477, A
14	79.5	7.2	139	4 US-09-621-976-5088	Sequence 5088, Ap
15	79.5	7.2	300	3 US-09-561-756-16	Sequence 36, Appl
16	79.5	7.2	300	3 US-09-227-721-36	Sequence 36, Appl
17	79.5	7.2	300	4 US-09-954-697-36	Sequence 36, Appl
18	79.5	7.2	315	2 US-08-484-956-91	Sequence 91, Appl
19	79.5	7.2	315	2 US-08-757-653-91	Sequence 91, Appl
20	79.5	7.2	315	3 US-08-520-946-91	Sequence 91, Appl
21	79.5	7.2	315	4 US-09-655-378A-91	Sequence 91, Appl
22	79.5	7.2	1010	4 US-09-654-449-2	Sequence 2, Appl
23	78.5	7.1	243	4 US-09-543-681A-7356	Sequence 7356, Ap
24	77	6.9	225	4 US-09-456-090A-94	Sequence 94, Appl
25	77	6.9	225	4 US-09-453-234-94	Sequence 94, Appl
26	76	6.9	229	4 US-09-546-043-8	Sequence 8, Appl
27	76	6.9	338	4 US-09-546-043-4	Sequence 4, Appl

28	76	6.9	546	3 US-09-457-040B-24	Sequence 24, Appl
29	76	6.9	546	4 US-09-538-092-668	Sequence 668, Appl
30	75.5	6.8	323	3 US-08-816-977-21	Sequence 21, Appl
31	75.5	6.8	323	4 US-09-334-477-21	Sequence 21, Appl
32	75	6.8	225	4 US-09-456-090A-58	Sequence 58, Appl
33	75	6.8	225	4 US-09-453-234-58	Sequence 58, Appl
34	75	6.8	454	4 US-09-450-209-16	Sequence 16, Appl
35	75	6.8	738	3 US-08-989-385-1	Sequence 1, Appl
36	75	6.8	738	4 US-09-593-826-1	Sequence 1, Appl
37	74.5	6.7	316	4 US-09-387-375-9	Sequence 9, Appl
38	74.5	6.7	316	4 US-10-041-400A-9	Sequence 9, Appl
39	74	6.7	225	4 US-09-456-090A-54	Sequence 54, Appl
40	74	6.7	225	4 US-09-456-090A-56	Sequence 56, Appl
41	74	6.7	225	4 US-09-456-090A-60	Sequence 60, Appl
42	74	6.7	225	4 US-09-456-090A-62	Sequence 62, Appl
43	74	6.7	225	4 US-09-456-090A-66	Sequence 66, Appl
44	74	6.7	225	4 US-09-456-090A-68	Sequence 68, Appl
45	74	6.7	225	4 US-09-456-090A-70	Sequence 70, Appl

ALIGNMENTS

RESULT 1
US-08-729-152-8
Sequence 8, Application US/08729152
Patent No. 5871739
GENERAL INFORMATION:
APPLICANT: Inoue, Eri
TITLE OF INVENTION: Pharmaceutical Composition
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSER: Wenderoch, Lind & Ponack
STREET: Southern Building, Suite 700, 805 Fifteenth
STREET: Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,152
FILING DATE: 11-OCT-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 291993/1995
FILING DATE: 13-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
US-08-729-152-8
Query Match 27.1%, Score 300, DB 2, Length 205;
Best Local Similarity 37.1%, Pred. No. 2, 4e-24;
Matches 63; Conservative 31; Mismatches 72; Indels 4; Gaps 3;

Qy 8 EDRCGFQHYGSCNDCPNL-QPYFRCNSIRVLSCGMVLYERPNYQGHQYFLRBDYDY 66
Db 23 EBNQSHSHLNGCPCPNKGTVEKASVLVQAPPMWQAGPQKGFVFEKKEYPW 82
Qy 67 OQMGF--NDSIRSCRLIPQHTGFRMRIRYERDPRQMS-ITDCPSLDRFLTEVH 123
Db 83 DSWTSRRRTDLSLRPIKVDQEHKILYENPNFTGKMKELIDDVSPFAHGYQENVS 142
Qy 124 SLNVLEGSWVLYEMSYRGROYLLRPGYRRRLDMGANAKYGLRRMD 173
Db 143 SVRVSGTWGYQYGRGLQYLLEKGDYKOSDFGAPHPQVQSVRRIRD 192

RESULT 2
US-08-729-152-1
Sequence 1, Application US/08729152
Patent No. 5871739
GENERAL INFORMATION:
APPLICANT: Inoue, Eri
TITLE OF INVENTION: Pharmaceutical Composition
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: Southern Building, Suite 700, 805 Fifteenth
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,152
FILING DATE: 11-OCT-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 291993/1995
FILING DATE: 13-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
US-08-729-152-1

Query Match 25.4%; Score 281.5; DB 2; Length 215;
Best Local Similarity 34.1%; Pred. No. 2.5e-22;
Matches 64; Conservative 37; Mismatches 70; Indels 13; Gaps 6;

Qy 3 RIKFKEDRGFGHYGSCNDCPNL-QPYFRCNSIRVLSCGMVLYERPNYQGHQYFLRBDY 61
Db 32 KITIYDENQGMKMEFTSSCPNVSESRFNVASLKVESGAMTGYEHTSCGQFLERK 91
Qy 62 DYEDYQGMGPN---DSIRSCR-LIPQHTGFRMRIRYERDPRQMS-ITDCPSLDRFLTEVH 116
Db 92 EYRPMWAGSGSNVYHMERLMSFRPFCSANHKESKMTIFEKENFGRQWEISDDYPSLQAM 151
Qy 117 -PHLTHSHSNVLEGSWVLYEMSYRGROYLLR---PGEYRYLDMG--ANNAKYGSIR 169

Db 152 GWRNEVGSNKIOGAWCYHYLGRNGYQYLKCDHHEGDYKAWREWSHAQTSQISIR 211
Qy 170 RV 171
Db 212 RI 213

RESULT 3
US-08-664-449-39
Sequence 39, Application US/08664449
Patent No. 5766905
GENERAL INFORMATION:
APPLICANT: Studier, F. W.
TITLE OF INVENTION: Cytoplasmic Bacteriophage Display System
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brookhaven National Laboratory
STREET: Building 902C
CITY: Upton
STATE: NY
COUNTRY: US
ZIP: 11973
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/664,449
FILING DATE: 17-June-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bogosian, Margaret
REGISTRATION NUMBER: 25,324
REFERENCE/DOCKET NUMBER: AUI-9618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 344-7338
TELEFAX: (516) 344-3729
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-664-449-39

Query Match 9.0%; Score 100; DB 1; Length 42;
Best Local Similarity 53.8%; Pred. No. 0.00095;
Matches 21; Conservative 0; Mismatches 0; Indels 18; Gaps 1;

Qy 177 DNSSSYVDKLAAL-----EHHHHH 197
Db 4 DPNSSVDKLAALAIKASOPELAPEDPEVEHHHHH 42

RESULT 4
US-08-979-847B-122
Sequence 122, Application US/08979847B
Patent No. 6582703
GENERAL INFORMATION:
APPLICANT: PERRON, HERVE
BESSEME, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BERNARD
GARSON, JEREMY
TIXE, PHILIP
TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES

NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847B
FILING DATE: 26-NO. 6582703-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELEPHONE: 703-836-6400
TELEFAX: 703-836-6400
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 122:
US-08-979-847B-122

Query Match 7.8%; Score 86; DB 4; Length 378;
Best Local Similarity 78.9%; Pred. No. 0.65;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 179 NSSSVDTLAAALEHHHHH 197
| : |||||
DB 360 NFKSLPRLAALAEHHHHH 378

RESULT 5
US-08-979-847B-121
Sequence 121, Application US/08979847B
Patent No. 6582703
GENERAL INFORMATION:
APPLICANT: PERRON, HERVE
BESIME, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMORIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BERNARD
GARSON, JEREMY
TUIKE, PHILIP
TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES
NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847B
FILING DATE: 26-NO. 6582703-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELEPHONE: 703-836-6400
TELEFAX: 703-836-6400
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 121:
US-08-979-847B-121

Query Match 7.8%; Score 86; DB 4; Length 398;
Best Local Similarity 78.9%; Pred. No. 0.69;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 179 NSSSVDTLAAALEHHHHH 197
| : |||||
DB 380 NFKSLPRLAALAEHHHHH 398

RESULT 6
US-08-757-653-163
Sequence 163, Application US/08757653
Patent No. 584369
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELEPHONE: (415) 397-8338
TELEFAX: (415) 705-8410
INFORMATION FOR SEQ ID NO: 163:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-757-653-163

Query Match 7.4%; Score 82; DB 2; Length 320;

Best Local Similarity 19.2%; Pred. No. 1.4;
Matches 43; Conservative 24; Mismatches 51; Indels 106; Gaps 9;
QY 71 GENDSIRSCRLIPQHT---GTFMRRI--YERDDFRGOMSE-----ITDD---CP 111
Db 106 GSEDFPRQALIKELVDLGLARLEVPGEADVLASLAKKAEKGEYVRILTADKDLQY 165
QY 112 SLQDRFHLTEVHSLNVLGSSWVLYEMPSYRGROYLLRPGERYRL----- 156
Db 166 LLSDRIHV--LHP---EGYLI--TPAWLMEKYGIRPDQWADYRALTGDESNDLPQYKG 216
QY 157 -----DWGANNAKVGLRRVWDFYSDPNSSVDKL----- 186
Db 217 IGKTARKLLEWGSLEALLKNDRLKPAIRREKILAHMODLKLSDWLAKVRTDPLEYDF 276
QY 187 -----AAALEHHHHH 197
Db 277 AKRREPDRERLRAFLERFGLSLHFGLLSPKALAEHHHHH 320

RESULT 7
US-08-823-516-61
Sequence 61, Application US/08823516
Patent No. 5994069
GENERAL INFORMATION:
APPLICANT: Hall, Jeff G.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Mast, Andrea L.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple
NUMBER OF SEQUENCES: 163
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823.516
FILING DATE: 24-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/01072
FILING DATE: 21-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/759,038
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,314
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/756,386
FILING DATE: 29-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02736
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-823-516-61

Query Match 7.4%; Score 82; DB 2; Length 320;
Best Local Similarity 19.2%; Pred. No. 1.4;
Matches 43; Conservative 24; Mismatches 51; Indels 106; Gaps 9;

QY 71 GENDSIRSCRLIPQHT---GTFMRRI--YERDDFRGOMSE-----ITDD---CP 111
Db 106 GSEDFPRQALIKELVDLGLARLEVPGEADVLASLAKKAEKGEYVRILTADKDLQY 165
QY 112 SLQDRFHLTEVHSLNVLGSSWVLYEMPSYRGROYLLRPGERYRL----- 156
Db 166 LLSDRIHV--LHP---EGYLI--TPAWLMEKYGIRPDQWADYRALTGDESNDLPQYKG 216
QY 157 -----DWGANNAKVGLRRVWDFYSDPNSSVDKL----- 186
Db 217 IGKTARKLLEWGSLEALLKNDRLKPAIRREKILAHMODLKLSDWLAKVRTDPLEYDF 276
QY 187 -----AAALEHHHHH 197
Db 277 AKRREPDRERLRAFLERFGLSLHFGLLSPKALAEHHHHH 320

RESULT 8
US-08-759-038-102
Sequence 102, Application US/08759038
Patent No. 6090543
GENERAL INFORMATION:
APPLICANT: Prudent, James R.
APPLICANT: Hall, Jeff G.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
APPLICANT: Dahlberg, James E.
TITLE OF INVENTION: Cleavage Of Nucleic Acids
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759.038
FILING DATE: 02-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 29-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02574
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 102:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 320 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-758-038-102

Query Match 7.4%; Score 82; DB 3; Length 320;
 Best Local Similarity 19.2%; Pred. No. 1.4;
 Matches 43; Conservative 24; Mismatches 51; Indels 106; Gaps 9;

QY 71 GFNDISCRIPHT---GTFMRKI--YERDDPRGQMS-----ITDD---CP 111
 DB 106 GSEDFPQALIKELVDLGLARLEVPGEYADVDLASLAKAEKEGYEVRILTDKDLQ 165
 QY 112 SLDRFPLTEVHSLNVLEGSWVLYEMPSYRGQYLRLPGCYRRYL----- 156
 DB 166 LLSDRIRH--LHP---EGYLI---TPAWLMEKYGLRPDQADYRALTGDES DNLPGVKG 216
 QY 157 -----DWGAMNAKVGSLRRVMDFYSDPNSSVDKL----- 186
 DB 217 IGEKTARKLLEWGSLEALLKNLDRLKPAIREKILAHMDLKLSDWLAKVRTDLPLEVD 276
 QY 187 -----AAALEHHHHH 197
 DB 277 AKRREPDERLRALFLERLEFGSLHFEGLLESPKAALEHHHHH 320

RESULT 9

US-08-758-314-102
 Sequence 102, Application US/08758314
 Patent No. 6090606

GENERAL INFORMATION:

APPLICANT: Kaiser, Michael W.

APPLICANT: Lyamichev, Victor I.

APPLICANT: Lyamichev, Natasha

TITLE OF INVENTION: Improved Cleavage Agents

NUMBER OF SEQUENCES: 134

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States Of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/758,314

FILING DATE: 02-DEC-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/

FILING DATE: 29-NOV-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/682,853

FILING DATE: 12-JUL-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/599,491

FILING DATE: 24-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: FORS-02575

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 102:

SEQUENCE CHARACTERISTICS:

LENGTH: 320 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-758-314-102

Query Match 7.4%; Score 82; DB 3; Length 320;
 Best Local Similarity 19.2%; Pred. No. 1.4;
 Matches 43; Conservative 24; Mismatches 51; Indels 106; Gaps 9;

QY 71 GFNDISCRIPHT---GTFMRKI--YERDDPRGQMS-----ITDD---CP 111
 DB 106 GSEDFPQALIKELVDLGLARLEVPGEYADVDLASLAKAEKEGYEVRILTDKDLQ 165
 QY 112 SLDRFPLTEVHSLNVLEGSWVLYEMPSYRGQYLRLPGCYRRYL----- 156
 DB 166 LLSDRIRH--LHP---EGYLI---TPAWLMEKYGLRPDQADYRALTGDES DNLPGVKG 216
 QY 157 -----DWGAMNAKVGSLRRVMDFYSDPNSSVDKL----- 186
 DB 217 IGEKTARKLLEWGSLEALLKNLDRLKPAIREKILAHMDLKLSDWLAKVRTDLPLEVD 276
 QY 187 -----AAALEHHHHH 197
 DB 277 AKRREPDERLRALFLERLEFGSLHFEGLLESPKAALEHHHHH 320

RESULT 10

US-09-684-938-102
 Sequence 102, Application US/09684938
 Patent No. 6555357

GENERAL INFORMATION:

APPLICANT: Kaiser, Michael W.

APPLICANT: Lyamichev, Victor I.

APPLICANT: Lyamichev, Natasha

TITLE OF INVENTION: Improved Cleavage Agents

FILE REFERENCE: FORS-03755

CURRENT APPLICATION NUMBER: US/09/684,938

CURRENT FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 09/308,825

PRIOR FILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: 08/757,653

PRIOR FILING DATE: 1996-11-29

PRIOR APPLICATION NUMBER: 08/758,314

PRIOR FILING DATE: 1996-12-02

PRIOR APPLICATION NUMBER: PCT/US97/21783

NUMBER OF SEQ ID NOS: 188

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 102

LENGTH: 320

TYPE: PRT

ORGANISM: Artificial Sequence

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-684-938-102

Query Match 7.4%; Score 82; DB 4; Length 320;
 Best Local Similarity 19.2%; Pred. No. 1.4;
 Matches 43; Conservative 24; Mismatches 51; Indels 106; Gaps 9;

QY 71 GFNDISCRIPHT---GTFMRKI--YERDDPRGQMS-----ITDD---CP 111
 DB 106 GSEDFPQALIKELVDLGLARLEVPGEYADVDLASLAKAEKEGYEVRILTDKDLQ 165
 QY 112 SLDRFPLTEVHSLNVLEGSWVLYEMPSYRGQYLRLPGCYRRYL----- 156
 DB 166 LLSDRIRH--LHP---EGYLI---TPAWLMEKYGLRPDQADYRALTGDES DNLPGVKG 216
 QY 157 -----DWGAMNAKVGSLRRVMDFYSDPNSSVDKL----- 186
 DB 217 IGEKTARKLLEWGSLEALLKNLDRLKPAIREKILAHMDLKLSDWLAKVRTDLPLEVD 276

QY 187 -----AAALEHHHHH 197
Db 277 AKRREPDRELRALFLERLEFGSLHHEFGLESPPKAALEHHHHH 320
US-09-940-244-61
RESULT 11
US-09-308-825A-102
Sequence 102, Application US/09308825A
Patent No. 6562611
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Improved Cleavage Agents
FILE REFERENCE: FORS-03755
CURRENT APPLICATION NUMBER: US/09/308,825A
PRIOR FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: 08/757,653
PRIOR FILING DATE: 1996-11-29
PRIOR APPLICATION NUMBER: 08/758,314
PRIOR FILING DATE: 1996-12-02
PRIOR APPLICATION NUMBER: PCT/US97/21763
PRIOR FILING DATE: 1997-11-29
NUMBER OF SEQ ID NOS: 188
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 102
LENGTH: 320
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-308-825A-102
Query Match 7.4%; Score 82; DB 4; Length 320;
Best Local Similarity 19.2%; Pred. No. 1.4;
Matches 43; Conservative 24; Mismatches 51; Indels 106; Gaps 9;
QY 71 GENDIRSCRLIPQHT---GTFMRRI--YERDDFGQMS-----ITDD---CP 111
Db 106 GSEDPFRLALIKELVLDLGLARLEVPGEADVLAASAKAEKEGEVRLITADKOLYQ 165
QY 112 SLQDRFHLTEVHSLNVLEGSWVLYEMPSYRGROYLAPGEYRRL----- 156
Db 166 LLSDRIHV--LHP-----EGYLI---TPAWLMEKTLGRPDQADYRALTGDESNDLPGVKG 216
QY 157 -----DWGAMNAKVSLLRRVMDFYSDPNSSVDKLT----- 186
Db 217 IGEKTARKLLEWGSLEALLKNLDRLKPAIREKILAMMDLKLSDLAQVTTDLPLEVD 276
QY 187 -----AAALEHHHHH 197
Db 277 AKRREPDRELRALFLERLEFGSLHHEFGLESPPKAALEHHHHH 320
RESULT 12
US-09-940-244-61
Sequence 61, Application US/09940244
Patent No. 6692817
GENERAL INFORMATION:
APPLICANT: Neri, Bruce P.
APPLICANT: Hall, Jeff G.
APPLICANT: Lyamichev, Victor
APPLICANT: Smith, Lloyd M.
TITLE OF INVENTION: Reactions on Dendrimers
FILE REFERENCE: FORS-06478
CURRENT APPLICATION NUMBER: US/09/940,244
CURRENT FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 422
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 61
LENGTH: 320
TYPE: PRF
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Synthetic
US-09-940-244-61
Query Match 7.4%; Score 82; DB 4; Length 320;
Best Local Similarity 19.2%; Pred. No. 1.4;
Matches 43; Conservative 24; Mismatches 51; Indels 106; Gaps 9;
QY 71 GENDIRSCRLIPQHT---GTFMRRI--YERDDFGQMS-----ITDD---CP 111
Db 106 GSEDPFRLALIKELVLDLGLARLEVPGEADVLAASAKAEKEGEVRLITADKOLYQ 165
QY 112 SLQDRFHLTEVHSLNVLEGSWVLYEMPSYRGROYLAPGEYRRL----- 156
Db 166 LLSDRIHV--LHP-----EGYLI---TPAWLMEKTLGRPDQADYRALTGDESNDLPGVKG 216
QY 157 -----DWGAMNAKVSLLRRVMDFYSDPNSSVDKLT----- 186
Db 217 IGEKTARKLLEWGSLEALLKNLDRLKPAIREKILAMMDLKLSDLAQVTTDLPLEVD 276
QY 187 -----AAALEHHHHH 197
Db 277 AKRREPDRELRALFLERLEFGSLHHEFGLESPPKAALEHHHHH 320

RESULT 13
US-09-270-767-43477
Sequence 43477, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 43477
LENGTH: 655
TYPE: PRF
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43477
Query Match 7.3%; Score 80.5; DB 4; Length 655;
Best Local Similarity 20.1%; Pred. No. 5.4;
Matches 42; Conservative 34; Mismatches 102; Indels 31; Gaps 8;
QY 3 RIKEKEDRGFGHGYSCNSDCNLPYFSRCSIRV--LSGCMLYERNYQGHQYFLR- 59
Db 180 QAKFNEKMFQVH-----DIETPDQVQLKIVEVEKTAGLHVESKQYKSOULEQP 233
QY 60 -----RGDYPDYQOMGFNDISRCRLIPQHTGTFMRRIYE--RDPRFGQSEITDDCP 111
Db 234 TEGVPTTKGDI-----VIFHITLPLERMMECH---PFLKCSMSNELLSATLVTSDLT 284
QY 112 SLQDRFHLTEVHSLNVLEGSWVLYEMPSYRGROYLAP---GEYRRLDWGAMNAKVS 167
Db 285 GSEGVHL-PIKSAKNADETLARLRLPYVAVOFQYYSPLDFKNTYAHYWPMSWPNLDVGH 343
QY 168 LRRVMDFYSDPNSSVDKLAALAEHHHHH 196
Db 344 RGNKSYIADAPARENTIASFLSHHHH 372
RESULT 14
US-09-621-976-5088
Sequence 5088, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jodert, S.


```

; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5088
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 104
; OTHER INFORMATION: Xaa = Ala,Asp
; NAME/KEY: UNSURE
; LOCATION: 114
; OTHER INFORMATION: Xaa = Ile,Ser
US-09-621-976-5088

```

Query Match 7.2%; Score 79.5; DB 4; Length 139;

Best Local Similarity 41.7%; Pred. No. 0.81;
Matches 20; Conservative 7; Mismatches 16; Indels 5; Gaps 2;

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QY      124 SLNVLEGSWVLYEMPYRGROYLRLPGERYRRLDGMN--AKVGSRLR 169
DB      45  SIVYKSGIWIYEGSNFLGRQILRLPNEIP--NWTAFSRWKTIGSLR 89

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RESULT 15

```

US-09-561-756-36
; Sequence 36 Application US/09561756
; Patent No. 6376226
; GENERAL INFORMATION:
; APPLICANT: Alimetil, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 480140.431
; CURRENT APPLICATION NUMBER: US/09/561,756
; CURRENT FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 09/227,721
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Rev-Caspase-6 constructed from human caspase-6
US-09-561-756-36

```

Query Match 7.2%; Score 79.5; DB 3; Length 300;

Best Local Similarity 31.5%; Pred. No. 2.3;
Matches 28; Conservative 10; Mismatches 22; Indels 29; Gaps 6;

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QY      128 LEGSWVLYEMPYRGROYLRLPGERYRRLDGMN---NAKVGSLRYMDPYSDPN---- 179
DB      35  VNGSWYIIDLCEMVGK-----YGSLEFTELTIVNRKV--SQRRV-DFCKDPSAIGK 84
QY      180 -----SSSVDKL-----AAALEHHHHH 197
DB      85  KQVPCFASMLTKLHFFPKSNLEHHHHH 113

```

Search completed: January 14, 2005, 12:06:50
Job time : 23 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	424.5	38.3	89	17	US-10-425-115-346968	Sequence 346968, A
2	320	28.9	616	15	US-10-108-260A-3095	Sequence 3095, A
3	320	28.9	781	10	US-09-865-050A-668	Sequence 668, App
4	257	23.2	197	17	US-10-723-860-1946	Sequence 1946, App
5	253	22.8	97	9	US-09-925-398-655	Sequence 655, App
6	253	22.8	97	14	US-10-102-806-655	Sequence 655, App
7	210.5	19.0	511	14	US-10-104-047-2339	Sequence 2339, App
8	200	18.1	138	14	US-10-106-698-5559	Sequence 5559, App
9	163	14.7	83	9	US-09-864-761-44293	Sequence 44293, A
10	147	13.3	30	9	US-09-808-002-62	Sequence 62, App1
11	123.5	11.1	826	15	US-10-395-241-18	Sequence 18, App1
12	123	11.1	168	14	US-10-360-053-2	Sequence 2, App1
13	123	11.1	168	14	US-10-360-053-4	Sequence 4, App1

15	14	119	10.7	21	14	US-10-010-160-68	Sequence 68, App
14	15	100.5	9.1	151	14	US-10-360-053-10	Sequence 10, App
16	15	100.5	9.1	159	14	US-10-360-053-12	Sequence 12, App
17	16	95	8.6	526	9	US-09-731-221-79	Sequence 79, App
18	18	93.5	8.4	381	14	US-10-141-531-49	Sequence 49, App
19	19	93.5	8.4	381	14	US-10-290-072-47	Sequence 47, App
20	20	93	8.4	516	9	US-09-804-626-4	Sequence 4, App
21	21	93	8.4	519	14	US-10-359-369-34	Sequence 34, App
22	22	92	8.3	381	14	US-10-141-531-48	Sequence 48, App
23	23	92	8.3	381	14	US-10-141-531-49	Sequence 49, App
24	24	92	8.3	381	14	US-10-141-531-50	Sequence 50, App
25	25	92	8.3	381	14	US-10-141-531-51	Sequence 51, App
26	26	92	8.3	381	14	US-10-141-531-52	Sequence 52, App
27	27	92	8.3	381	14	US-10-141-531-53	Sequence 53, App
28	28	92	8.3	381	14	US-10-141-531-54	Sequence 54, App
29	29	92	8.3	381	14	US-10-141-531-55	Sequence 55, App
30	30	92	8.3	381	14	US-10-141-531-58	Sequence 58, App
31	31	92	8.3	381	14	US-10-290-072-48	Sequence 48, App
32	32	92	8.3	381	14	US-10-290-072-49	Sequence 49, App
33	33	92	8.3	381	14	US-10-290-072-50	Sequence 50, App
34	34	92	8.3	381	14	US-10-290-072-51	Sequence 51, App
35	35	92	8.3	381	14	US-10-290-072-52	Sequence 52, App
36	36	92	8.3	381	14	US-10-290-072-53	Sequence 53, App
37	37	92	8.3	381	14	US-10-290-072-54	Sequence 54, App
38	38	92	8.3	381	14	US-10-290-072-55	Sequence 55, App
39	39	92	8.3	381	14	US-10-290-072-58	Sequence 58, App
40	40	92	8.3	481	14	US-10-141-531-59	Sequence 59, App
41	42	90.5	8.2	481	14	US-10-290-072-59	Sequence 59, App
42	42	90.5	8.2	481	14	US-10-369-493-5789	Sequence 5789, App
43	43	85	8.0	556	10	US-09-819-266-28	Sequence 28, App
44	44	85	8.0	559	10	US-09-819-266-25	Sequence 25, App
45	45	88	7.9	518	9	US-09-804-626-2	Sequence 2, App

ALIGNMENTS

```

RESULT 1
US-10-425-115-346968
; Sequence 346968, Application US/10425115
; Publication No. US2004021472A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-26
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO: 346968
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_79599C.1.pep
US-10-425-115-346968

```

Query Match	38.3%	Score 424.5;	DB 17;	Length 89;
Best Local Similarity	82.2%	Pred. No. 2.7e-36;		
Matches	74;	Conservative	6;	Mismatches 9; Indels 1; Gaps 1
QY	1	MGRIRKFKEDRFEQGHVYS	CNSD	CPYLQYF
		PFSS	CNS	IRVLSCGMM
		YERPNYGHQYFLRR		60
DB	1	MGRITFYEDRFGRCYECSSD	CPYLQYF	FRSCNSVRVDSGCM
		LYERNYGHQYFLRR		60
QY	61	GDYEDYQOMGPNDS	IRSCRLIP	QHTGTFRR
		90		
DB	61	GDYEDYQOMLGFS	DSIRSCRLIP	-HTGSHR
		89		

RESULT 2
 US-10-108-260A-3095
 ; Sequence 3095, Application US/10108260A
 ; Publication No. US20040005560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: No. US20040005560A1 full length cDNA
 ; FILE REFERENCE: H1-A0106
 ; CURRENT APPLICATION NUMBER: US/10/108,260A
 ; CURRENT FILING DATE: 2002-03-27
 ; NUMBER OF SEQ ID NOS: 5458
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 3095
 ; LENGTH: 616
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-108-260A-3095

Query Match 28.9%; Score 320; DB 15; Length 616;
 Best Local Similarity 33.0%; Pred. No. 2.4e-24;
 Matches 68; Conservative 34; Mismatches 78; Indels 26; Gaps 2;

QY 8 EDGFGQGHYHSCNSDCPNLQ-----PYFSRCNSIRVLSCGCMLYERPNOGHQYFLRR 60
 DB 129 EAPGFGQGSWEVSRIYVLQCPEDSQPHLASVGLRVLGCGCWYGEKEGFRGHQYLLER 188
 QY 61 GDYPYQOMMGFNDSIRSCRLIPQHTGTFMRIRYERDPRGQMSBITDDCSLDRPHLT 120
 DB 189 GEYFMSHMGYDELTLRLVIRIDFGDPVAVLFEANDFEHGVAVSALPDVDELVOHGP 248
 QY 121 EVHSINLVESGWSVLYEMPSYRGROYLLRPGYRRYLDGMANAKVGLRRVY----- 172
 DB -249 STQAIHVLSGWVAVYQEVGFGSEGVLEKGYVRNCEBWDGANSITLASIQVTLQVGBHDLH 308
 QY 173 -----DFYSDPSSSVDKLA 187
 DB 309 FVSKIQLFSPDFLGDHFSFPDDQA 334

RESULT 3
 US-09-866-050A-668
 ; Sequence 668, Application US/09866050A
 ; Publication No. US20030040471A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Strachan, Lorna
 ; APPLICANT: Sleeman, Matthew
 ; APPLICANT: Onrust, Rene
 ; APPLICANT: Marison, James G.
 ; APPLICANT: Kumble, Krishanand D.
 ; TITLE OF INVENTION: Compositions isolated from skin cells
 ; FILE REFERENCE: 11000.1011c4V
 ; CURRENT APPLICATION NUMBER: US/09/866,050A
 ; CURRENT FILING DATE: 2001-05-24
 ; NUMBER OF SEQ ID NOS: 725
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 668
 ; LENGTH: 781
 ; TYPE: PRT
 ; ORGANISM: Mouse
 ; US-09-866-050A-668

Query Match 28.9%; Score 320; DB 10; Length 781;
 Best Local Similarity 33.3%; Pred. No. 3.2e-24;
 Matches 64; Conservative 34; Mismatches 74; Indels 20; Gaps 2;

QY 8 EDGFGQGHYHSCNSDCPNLQ-----PYFSRCNSIRVLSCGCMLYERPNOGHQYFLRR 60
 DB 294 EAPGFGQGSWEVSRIYVLQCPEDSQPHLASVGLRVLGCGCWYGEKEGFRGHQYLLER 353
 QY 61 GDYPYQOMMGFNDSIRSCRLIPQHTGTFMRIRYERDPRGQMSBITDDCSLDRPHLT 120

DB 354 GEVADNSHMGYDELLTSLRVIRTDGDPVAVLFEEDMFGCHREVENSSALPDVELAQHGP 413
 QY 121 EVHSINLVESGWSVLYEMPSYRGROYLLRPGYRRYLDGMANAKVGLRRV----- 171
 DB 414 STQAIHVLSGWVAVYERVFGSGEYVLEKGVYRNCDWGSNCALSLQVYVQVGSBDLH 473
 QY 172 -----MDYSDPN 179
 DB 474 FVTKIQLFSGPN 485

RESULT 4
 US-10-723-860-1946
 ; Sequence 1946, Application US/10723860
 ; Publication No. US20040253606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Ginsburg, Wendy M.
 ; APPLICANT: Zlotnik, Albert
 ; TITLE OF INVENTION: Methods of diagnosis of Soft Tissue Sarcoma, Compositions &
 ; FILE REFERENCE: 05882.0193.NPUS01
 ; CURRENT APPLICATION NUMBER: US/10/723,860
 ; CURRENT FILING DATE: 2003-11-26
 ; PRIOR APPLICATION NUMBER: 60/429,739
 ; NUMBER OF SEQ ID NOS: 8393
 ; SOFTWARE: Patent In version 3.2
 ; SEQ ID NO 1946
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-723-860-1946

Query Match 23.2%; Score 257; DB 17; Length 197;
 Best Local Similarity 34.6%; Pred. No. 2.1e-18;
 Matches 62; Conservative 35; Mismatches 66; Indels 16; Gaps 7;

QY 8 EDGFGQGHYHSCNSDCPNLQ-----PYFSRCNSIRVLSCGCMLYERPNOGHQYFLRRDYPD 65
 DB 18 DEEDFGRCRLISDANVCERGLPRVSVVGVGWVAFYPPFGQGFLEKGDYPR 77
 QY 66 YQOMGF---NDSIRSCR--LIPQHTGTFMRIRYERDPRGQMSBITDDCSLDR-PH 118
 DB 78 WSAMSGSSHSNNGQLSPRPVLCANHNS-RVTLFEGDNFGQCKRDVVDYISLPSMGWA 136
 QY 119 LTVHSINLVESGWSVLYEMPSYRGROYLL---RPGYRRYLDWG--ANNAVGLRRV 171
 DB 137 SKDVGLKVSAGWAVYQYFGYGVYVLERDRHSGEFTYGLGTQAHGQLOGISRRV 195

RESULT 5
 US-09-925-298-655
 ; Sequence 655, Application US/09925298
 ; Publication No. US20020039764A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA103
 ; CURRENT APPLICATION NUMBER: US/09/925,298
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05881
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 846
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 655
 ; LENGTH: 97
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE: SITE
 ; NAME/KEY: SITE

LOCATION: (38)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (91)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-925-298-655

Query Match 22.8%; Score 253; DB 9; Length 97;
 Best Local Similarity 51.2%; Pred. No. 2.3e-18;
 Matches 41; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

QY 3 RIKKEDRGFGHYHSCNSDCPNLQPYFRCNSIRVLSCMMLYERPNYQHQYFLRGD 62
 DB 15 QITREYDKNFGGRYDDCCDCAHXHTYLSRCNSIKVEGTVAYERPFAGYMTLLPQGE 74

QY 63 YPDYQOMWGFNDIRSCLRI 82
 DB 75 YPEYQRMWGLNDRILSSKRAV 94

RESULT 6
 US-10-102-806-655

Sequence 655, Application US/10102806
 Publication No. US20030054421A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 FILE REFERENCE: PA103P1C1
 CURRENT APPLICATION NUMBER: US/10/102,806
 CURRENT FILING DATE: 2002-03-22
 PRIOR APPLICATION NUMBER: 09/925,298
 PRIOR FILING DATE: 2001-08-10
 PRIOR APPLICATION NUMBER: PCT/US00/05881
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: 60/124,270
 PRIOR FILING DATE: 1999-03-12
 NUMBER OF SEQ ID NOS: 846
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 655
 LENGTH: 97
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (38)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 NAME/KEY: SITE
 LOCATION: (91)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-10-102-806-655

Query Match 22.8%; Score 253; DB 14; Length 97;
 Best Local Similarity 51.2%; Pred. No. 2.3e-18;
 Matches 41; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

QY 3 RIKKEDRGFGHYHSCNSDCPNLQPYFRCNSIRVLSCMMLYERPNYQHQYFLRGD 62
 DB 15 QITREYDKNFGGRYDDCCDCAHXHTYLSRCNSIKVEGTVAYERPFAGYMTLLPQGE 74

QY 63 YPDYQOMWGFNDIRSCLRI 82
 DB 75 YPEYQRMWGLNDRILSSKRAV 94

RESULT 7
 US-10-104-047-2339
 Sequence 2339, Application US/10104047
 Publication No. US20030236392A1
 GENERAL INFORMATION:
 APPLICANT: HELIX RESEARCH INSTITUTE
 TITLE OF INVENTION: NO. US20030236392A1e1 full length cDNA
 FILE REFERENCE: H1-A0105
 CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT FILING DATE: 2002-03-25
 PRIOR APPLICATION NUMBER:
 PRIOR FILING DATE:
 NUMBER OF SEQ ID NOS: 4096
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2339
 LENGTH: 511
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-104-047-2339

Query Match 19.0%; Score 210.5; DB 14; Length 511;
 Best Local Similarity 30.1%; Pred. No. 4.9e-13;
 Matches 43; Conservative 33; Mismatches 66; Indels 1; Gaps 1;

QY 30 FSRCSIRVLSCMMLYERPNYQHQYFLRGDYPDYQOMWGFNDIRSCLRIPOHTGTF 89
 DB 54 FHRIGSIRVLGVVAVAYEKHFQGOFLLEGDFEDNACGALSPILSFYIOLANFTES 113

QY 90 RMRIYERDDPRGOWSEITD-DCPSLQDRFHLTEVHSLNVLGSAVLYEMPSYRGROYLLR 148
 DB 114 SVTLFESDLSGKFTIDITNOEISDLSEIGSGSKTRSIHVASGVWAVYQKFFGGEYITLE 173

QY 149 PGEYRRLDWGANNAKVSRLRV 171
 DB 174 KGKTKCFDWCSSNNIMISIRPI 196

RESULT 8
 US-10-106-698-5959

Sequence 5959, Application US/10106698
 Publication No. US20030109690A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
 FILE REFERENCE: PA005P1
 CURRENT APPLICATION NUMBER: US/10/106,698
 CURRENT FILING DATE: 2002-03-27
 PRIOR APPLICATION NUMBER: PCT/US00/26524
 PRIOR FILING DATE: 2000-09-28
 PRIOR APPLICATION NUMBER: US 60/157,137
 PRIOR FILING DATE: 1999-09-29
 PRIOR APPLICATION NUMBER: US 60/163,280
 PRIOR FILING DATE: 1999-11-03
 NUMBER OF SEQ ID NOS: 8564
 SOFTWARE: PatentIn Ver. 3.0
 SEQ ID NO 5959
 LENGTH: 138
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-106-698-5959

Query Match 18.1%; Score 200; DB 14; Length 138;
 Best Local Similarity 36.0%; Pred. No. 1.2e-12;
 Matches 49; Conservative 26; Mismatches 47; Indels 14; Gaps 6;

QY 49 PNYGHOYFLRGRYPDYQOMGF----NDSIRCR--LIPQHTGRMRRIYEDDPRGQ 102
 DB 2 PDPQGOQFIEKGYPPWASGSSSHNSNQLSFRPYLCANHDS--RVTLFEBDNFGC 60

QY 103 MSEITDQPSLQDR-FHLTEVHSLNVLGSAVLYEMPSYRGROYLL--RPGYRRLYLD 157
 DB 61 KFDLVDDYPSLPSGMSKDVGSILKSSGAWAVYQYGRGYQYVLERRDRSGEFCTYGE 120

QY 158 WG--AMNAKVSRLRV 171
 DB 121 LGTAHTGQLQGSIRRV 136

RESULT 9
 US-09-864-761-44293
 Sequence 44293, Application US/09864761
 Patent No. US20020048763A1

```

; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 44293
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC00596.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.95
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.94
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.95
; OTHER INFORMATION: SWISSPROT HIT: P26444, EVALUE 8.00e-19
; OTHER INFORMATION: EST_HUMAN HIT: A1142108.1, EVALUE 4.00e-14
; US-09-864-761-44293

Query Match 14.7%; Score 163; DB 9; Length 83;
Best Local Similarity 38.0%; Pred. No. 4.4e-09;
Matches 30; Conservative 13; Mismatches 34; Indels 2; Gaps 1;
4 IKFKEDRGFOQHYSNCSDCPNLQP--YFSRCNSIRVLSCGMILYERPNYQGHQYFLRRG 61
Db 1 ITVEGHNFTGQKLEVGDCNPFQDRGFNRKRVNSIHVESGAMVCFNHPDRGQQLFLEHG 60
QY 62 DYDPYQGMGPNDSRSCR 80
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Db 61 DYDPFFRNSSHSDMGSCR 79
RESULT 10
; Sequence 62, Application US/09808602
; Patent No. US20020155115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herrman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: No. US20020155115A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-808-602-62

Query Match 13.3%; Score 147; DB 9; Length 30;
Best Local Similarity 90.0%; Pred. No. 5.7e-08;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
140 YRGROYLRGGEYRRYLDGMAKVGSLR 169
Db 1 YRGROYLRGGEYRRYLDGMAKVGSPR 30

RESULT 11
; Sequence 18, Application US/10395241
; Publication No. US20040038367A1
; GENERAL INFORMATION:
; APPLICANT: YAOI, Katsuro
; APPLICANT: MITSUISHI, Yasushi
; TITLE OF INVENTION: NOVEL XYLOGLUCAN OLIGOSACCHARIDE-DEGRADING ENZYME, POLYNUCLEOTIDE
; FILE REFERENCE: 073756
; CURRENT APPLICATION NUMBER: US/10/395,241
; CURRENT FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: JP 2002-83433
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Xyloglucan Oligosaccharide-Degrading Enzyme with Histidine Tag
; US-10-395-241-18

Query Match 11.1%; Score 123.5; DB 15; Length 826;
Best Local Similarity 30.2%; Pred. No. 0.001;
Matches 39; Conservative 10; Mismatches 41; Indels 39; Gaps 4;
93 IYERDDFRQGMSEITDDCPSLQDRFHLTEVHSLNVLGSGWVLYEMPSYRGROYLLRPGY 152
Db 713 LYRSDNGSTWTRVND-----QEHNY--GPTWLEADPKYGVGYLTGNGRG 757
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QY 153 RRYLDW-----GANNAYGS-----LRRVNDFYSDPNSSVDKLA 188
DB 758 IIVYADLTNRKSNBEKSTAKCANQKGTCHYVKEIIVFWPCHAVPWLSDPNSSVDKLA 817
QY 189 ALEHHHHHH 197
DB 818 ALEHHHHHH 826

RESULT 12
US-10-360-053-2
; Sequence 2, Application US/10360053
; Publication No. US20030170230A1
; GENERAL INFORMATION:
; APPLICANT: Caterer, Nigel
; APPLICANT: Uttenchal, Lars O
; APPLICANT: Nielsen, Rasmus W
; TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antibiotic
; TITLE OF INVENTION: Fragments via Antiparallel Heterogeneous Coiled-Coil Peptide Regi
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: IMX-0028
; CURRENT APPLICATION NUMBER: US/10/360,053
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US60/354,376
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-360-053-2

Query Match 11.1%; Score 123; DB 14; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 SDPNSSVDKLAALAEHHHHHH 197
DB 147 SDPNSSVDKLAALAEHHHHHH 168

RESULT 13
US-10-360-053-4
; Sequence 4, Application US/10360053
; Publication No. US20030170230A1
; GENERAL INFORMATION:
; APPLICANT: Caterer, Nigel
; APPLICANT: Uttenchal, Lars O
; APPLICANT: Nielsen, Rasmus W
; TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antibiotic
; TITLE OF INVENTION: Fragments via Antiparallel Heterogeneous Coiled-Coil Peptide Regi
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: IMX-0028
; CURRENT APPLICATION NUMBER: US/10/360,053
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US60/354,376
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-360-053-4

Query Match 11.1%; Score 123; DB 14; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.00016;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 SDPNSSVDKLAALAEHHHHHH 197
DB 147 SDPNSSVDKLAALAEHHHHHH 168

RESULT 14
US-10-010-160-68
; Sequence 68, Application US/10010160
; Publication No. US20030103999A1
; GENERAL INFORMATION:
; APPLICANT: Rosey, Everett L.
; APPLICANT: Struggnell, Richard A.
; APPLICANT: Good, Robert T.
; APPLICANT: King, Kendall W.
; TITLE OF INVENTION: NOVEL THERAPEUTIC COMPOSITIONS FOR
; TITLE OF INVENTION: TREATING INFECTION BY LAMSONIA SPP.
; FILE REFERENCE: DAVI110.001AUS
; CURRENT APPLICATION NUMBER: US/10/010,160
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: AU PR1381
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/249,596
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide
US-10-010-160-68

Query Match 10.7%; Score 119; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 DPNSSVDKLAALAEHHHHHH 197
DB 1 DPNSSVDKLAALAEHHHHHH 21

RESULT 15
US-10-360-053-10
; Sequence 10, Application US/10360053
; Publication No. US20030170230A1
; GENERAL INFORMATION:
; APPLICANT: Caterer, Nigel
; APPLICANT: Uttenchal, Lars O
; APPLICANT: Nielsen, Rasmus W
; TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antibiotic
; TITLE OF INVENTION: Fragments via Antiparallel Heterogeneous Coiled-Coil Peptide Regi
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: IMX-0028
; CURRENT APPLICATION NUMBER: US/10/360,053
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US60/354,376
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-360-053-10

Query Match 9.1%; Score 100.5; DB 14; Length 151;
Best Local Similarity 50.0%; Pred. No. 0.031;
Matches 20; Conservative 2; Mismatches 7; Indels 11; Gaps 1;

Fri Jan 14 14:11:40 2005

us-10-030-605a-21.rapb

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Qy      158  WGANNAKTSLLRVDVFSDPNSSGVDKLAALENNHNH 197
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Db      123  WEALAKAKASQRRQ-----DVDRKLAALENNHNH 151

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Search completed: January 14, 2005, 12:13:02
Job time : 146 secs